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METHODS OF IDENTIFYING MODULATORS OF BROMODOMAINS

FIELD OF THE INVENTION

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The present invention provides the three-dimensional structure of a histone acetyltransferase bromodomain. The three-dimensional structural information is included in the invention. The present invention also identifies for the first time, that bromodomains can bind to an acetylated binding partners. The interaction between bromodomains and their binding partners play a crucial role in various cellular functions, including in the regulation/modulation of DNA transcription. Therefore, the present invention provides procedures for identifying agents that can modulate the interaction of bromodomains and their binding partners by high throughput drug screening and/or through the use of rational drug design based on the three-dimensional data provided herein.

BACKGROUND OF THE INVENTION

In recent years great strides have been made in the elucidation of the steps involved in 20 intercellular and intracellular signaling. Indeed, the individual steps of the cascade of events involved in a number of cellular signal transduction processes have been determined. For example, intercellular signal transduction generally begins with an intercellular ligand binding the extracellular portion of a receptor of the plasma membrane. The bound receptor then either directly or indirectly initiates the activation of one or more cellular factors. An activated cellular factor may act as 25 transcription factor by entering the nucleus to interact with its corresponding genomic response element, or alternatively, it may interact with other cellular factors depending on the complexity of the process. In either case, one or more transcription factors ultimately bind to one or more specific genomic response elements. This 30 binding plays a crucial role in the up and/or down regulation of the transcription of the specific genes that are under the control of these genomic response elements. However, the process of re-organizing the chromatin of eukaryotic cells, which is a prerequisite for the binding of the transcription factor to the genomic response elements, has remained a mystery.

Chromatin contains several highly conserved histone proteins including: H3, H4, H2A, H2B, and H1. These histone proteins package eukaryotic DNA into repeating nucleosomal units that are folded into higher-order chromatin fibers [Luger and Richmond, Curr. Opin. Genet. Dev. 8:140-146 (1998)]. A portion of the histone that comprises roughly a quarter of the protein protrudes from the chromatin surface, and is thereby sensitive to proteolytic enzymes [van Holde, in Chromatin (Rich, A,. ed., Springer, New York) pages111-148 (1988); Hect et al., Cell 80:583-592 (1995)]. This portion of the histone is known as the "histone tail". Histone tails tend to be free for protein-protein interaction, and are also the portion of the histone most prone to post-translational modification. Such post-translational modification includes acetylation, phosphorylation, methylation, ubiquitination, and ADP-ribosylation [van Holde, in Chromatin (Rich, A,. ed., Springer, New York) pages111-148 (1988)].

Of all classes of proteins, histones are amongst the most susceptible to posttranslational modification. Perhaps the best studied post-translational modification of
histones is the acetylation of specific lysine residues [Grunstin, M., Nature, 389:349352 (1997)]. Indeed, acetylation of histone lysine residues has been suggested to
play a pivotal role in chromatin remodeling and gene activation. Consistently,
distinct classes of enzymes, namely histone acetyltransferases (HATs) and histone
deacetylases (HDACs), acetylate or de-acetylate specific histone lysine residues
[Struhl, Genes Dev. 12:599-606 (1998)].

Nearly all known nuclear HATs contain an approximately 110 amino acid sequence
known as the bromodomain [Jeanmougin et al., Trends in Biochemical Sciences,
22:151-153 (1997)], a protein motif that was initially discovered in Drosophila
brahma protein. Bromodomains are found in a large number of chromatin-associated
proteins and have now been identified in approximately 40 proteins, often adjacent to
other protein motifs [Jeanmougin et al., Trends in Biochemical Sciences, 22:151-153
(1997); Tamkun et al., Cell, 68:561-572 (1992): Hanes et al., Nucleic Acids Research,
20:2603 (1992)]. Proteins that contain a bromodomain often contain a second
bromodomain. However, despite the wide occurrence of bromodomains and their

likely role in chromatin regulation, their three-dimensional structure and binding partners heretofore have remained unknown.

Therefore, there is a need to identify a binding partner for a bromodomain. In addition, there is a need to identify agonists or antagonists to the bromodomain-binding partner complex. Since a preferred method of drug-screening relies on structure based drug design, there is also a need to determine the three-dimensional structure of a bromodomain. In this case, once the three dimensional structure of bromodomain is determined, potential agonists and/or potential antagonists can be designed with the aid of computer modeling [Bugg et al., Scientific American, Dec.:92-98 (1993); West et al., TIPS, 16:67-74 (1995); Dunbrack et al., Folding & Design, 2:27-42 (1997)]. However, heretofore the three-dimensional structure of the bromodomain has remained unknown. Therefore, there is a need for obtaining a form of the bromodomain that is amenable for NMR analysis and/or X-ray crystallographic analysis. Furthermore, there is a need for the determination of the three-dimensional structure of the bromodomain. Finally, there is a need for procedures for related structural based drug design predicated on such structural data.

The citation of any reference herein should not be construed as an admission that such reference is available as "Prior Art" to the instant application.

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SUMMARY OF THE INVENTION

25 lysine residues of proteins. The present invention also provides the three-dimensional structure of a bromodomain as well as the three-dimensional structure of a bromodomain-acetyl-histamine complex. The structural information provided can be employed in methods of identifying drugs that can modulate the cellular processes that involve bromodomain-acetyl-lysine interactions. These interactions include chromatin remodeling, which is a required step in eukaryotic transcription. In a particular embodiment, the three-dimensional structural information is used in the design of an inhibitor of leukemia.

The present invention provides an isolated nucleic acid that encodes a peptide consisting of about 21 to 40 amino acids that comprises a ZA loop of a bromodomain. In a preferred embodiment the peptide comprises about 23 to 34 amino acids. The isolated nucleic acid can further comprise a heterologous nucleotide sequence.

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In a preferred embodiment the peptide comprises the amino acid sequence of SEQ ID NO:3. In another embodiment the peptide comprises the amino acid sequence of SEQ ID NO:43. In particular embodiments the ZA loop is obtained from the bromodomain having the amino acid sequence of SEQ ID NO:7, or SEQ ID NO:8, or SEQ ID NO:9, or SEQ ID NO:10, or SEQ ID NO:11, or SEQ ID NO:12, or SEQ ID NO:13, or SEQ ID NO:14, or SEQ ID NO:15, or SEQ ID NO:16, or SEQ ID NO:17, or SEQ ID NO:18, or SEQ ID NO:19, or SEQ ID NO:20, or SEQ ID NO:21, or SEQ ID NO: 22, or SEQ ID NO:23, or SEQ ID NO:24, or SEQ ID NO:25, or SEQ ID NO:26, or SEQ ID NO:27, or SEQ ID NO:28, or SEQ ID NO:29, or SEQ ID NO:30, or SEQ ID NO: or SEQ ID NO:31, or SEQ ID NO:32, or SEQ ID NO:33, or SEQ ID NO:34, or SEQ ID NO:35, or SEQ ID NO:36, or SEQ ID NO:37, or SEQ ID NO:38, or SEQ ID NO: or SEQ ID NO:39, or SEQ ID NO:40, or SEQ ID NO:41, or SEQ ID NO:42.

The present invention further provides a recombinant DNA molecule that comprises
an isolated nucleic acid of the present invention, as described above, with or without a
heterologous nucleotide sequence. Such a recombinant DNA molecule can be
operatively linked to an expression control sequence and can be part of an expression
vector. The present invention further provides a cell that comprises such an
expression vector. The cell can be either a eukaryotic or a prokaryotic cell. The
present invention further provides a method of expressing the peptides of the present
invention or fragments thereof in this cell. One such method comprises culturing the
cell in an appropriate cell culture medium under conditions that provide for
expression of the peptide by the cell.

The present invention further provides a peptide consisting of about 21 to 40 amino acids that comprises a ZA loop of a bromodomain. In a preferred embodiment the

peptide comprises about 23 to 34 amino acids. The present invention also provides fusion proteins or peptides comprising these peptides.

In a preferred embodiment the peptide comprises the amino acid sequence of SEQ ID NO:3. In another embodiment the peptide comprises the amino acid sequence of SEQ ID NO:43. In particular embodiments the ZA loop is obtained from the bromodomain having the amino acid sequence of SEQ ID NO:7, or SEQ ID NO:8, or SEQ ID NO:9, or SEQ ID NO:10, or SEQ ID NO:11, or SEQ ID NO:12, or SEQ ID NO:13, or SEQ ID NO:14, or SEQ ID NO:15, or SEQ ID NO:16, or SEQ ID NO:17, or SEQ ID NO:18, or SEQ ID NO:19, or SEQ ID NO:20, or SEQ ID NO:21, or SEQ ID NO: 22, or SEQ ID NO:23, or SEQ ID NO:24, or SEQ ID NO:25, or SEQ ID NO:26, or SEQ ID NO:27, or SEQ ID NO:28, or SEQ ID NO:29, or SEQ ID NO:30, or SEQ ID NO: or SEQ ID NO:31, or SEQ ID NO:32, or SEQ ID NO:33, or SEQ ID NO:34, or SEQ ID NO:35, or SEQ ID NO:36, or SEQ ID NO:37, or SEQ ID NO:38, or SEQ ID NO:

The present invention also provides antibodies raised against the peptides/proteins of the present invention, or raised against an antigenic fragment of these proteins/fragments. In a particular embodiment an antibody is raised against a

20 fragment of the ZA loop of a bromodomain. In another embodiment an antibody is raised against a fragment of a protein or peptide that comprises an acetyl-lysine, wherein the protein or peptide can bind to a bromodomain. Such fragments can be conjugated to a carrier protein or be part of a fusion protein. In one embodiment the antibody is a polyclonal antibody. In another embodiment, the antibody is a monoclonal antibody. A hybridoma that makes the monoclonal antibody is also part of the present invention. In a particular embodiment the antibody is a chimeric antibody. Antibodies that can specifically recognize acetyl-lysine residues involved bromodomain binding are also part of the present invention.

In another aspect of the present invention a method is provided for identifying a compound that modulates the affinity of a bromodomain for a ligand (and/or protein) that comprises an acetylated lysine. One such embodiment comprises contacting the

bromodomain and the ligand in the presence of a compound under conditions that, the bromodomain and the ligand bind in the absence of the compound. The affinity of the bromodomain for the ligand is then determined (e.g., measured). A compound is identified as a compound that modulates the affinty of the bromodomain for the ligand when there is a change in the affinity of the bromodomain for the ligand in the presence of the compound. When the affinity of the bromodomain for the ligand increases in the presence of the compound, the compound is identified as a promoting agent for the bromodomain-ligand complex. When the affinity of the bromodomain for the ligand decreases in the presence of the compound, the compound is identified as an inhibitor of the bromodomain-ligand complex. In a preferred embodiment, the compound to be tested is pre-selected by performing rational drug design with the set of atomic coordinates obtained from one or more of Tables 1-6. More preferably the selecting is performed in conjunction with computer modeling. In a particular embodiment, the compound is selected by performing rational drug design with the set of atomic coordinates obtained from a set of atomic coordinates defining the threedimensional structure of a bromodomain consisting of the amino acid sequence of SEQ ID NO:7 alone or with acetyl-histamine.

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The present invention also provides a method of identifying a compound that modulates the stability of a bromodomain-acetyl-lysine binding complex. One such 20 embodiment comprises contacting the bromodomain-acetyl-lysine binding complex in the presence of the compound under conditions in which the bromodomain-acetyllysine binding complex forms in the absence of the compound. The stability of the bromodomain-acetyl-lysine binding complex is then determined (e.g., measured). A 25 compound is identified as a compound that modulates the stability of the bromodomain-acetyl-lysine binding complex, when there is a change in the stability of the bromodomain-acetyl-lysine binding complex in the presence of that compound. When the stability of the bromodomain-acetyl-lysine binding complex increases in the presence of the compound, the compound is identified as a stabilizing agent. When 30 the stability of the bromodomain-acetyl-lysine binding complex decreases in the presence of the compound, the compound is identified as an inhibitor. In a preferred embodiment, the compound to be tested is pre-selected by performing rational drug

design with the set of atomic coordinates obtained from one or more of Tables 1-6. More preferably the selecting is performed in conjunction with computer modeling. In a particular embodiment, the compound is selected by performing rational drug design with the set of atomic coordinates obtained from a set of atomic coordinates defining the three-dimensional structure of a bromodomain consisting of the amino acid sequence of SEQ ID NO:7 alone or with acetyl-histamine.

As anyone having skill in the art of drug development would readily understand, the potential drugs selected by the above methodologies can be refined by re-testing in appropriate drug assays, including those disclosed herein. Chemical analogs of such potential drugs can be obtained (either through chemical synthesis or drug libraries) and be analogously tested. Therefore, methods comprising successive iterations of the steps of the individual drug assays, as exemplified herein, using either repetitive or different binding studies, or transcription activation studies or other such studies are envisioned in the present invention. In addition, potential drugs may be identified first by rapid throughput drug screening, as described below, prior to performing computer modeling on a potential drug using the three-dimensional structure of the bromodomain.

The present invention further comprises all of the potential, selected, and putative compounds (drugs) identified by the methods of the present invention, as well as the final drugs themselves identified with the methods of the present invention.

The present invention further provides a method for identifying a potential binding
partner for a protein (e.g., a histone) comprising an acetyl-lysine. One such embodiment comprises contacting the protein with a polypeptide comprising a bromodomain. In a preferred embodiment the bromodomain comprises the amino acid sequence of SEQ ID NO:3. In particular embodiments the bromodomain has the amino acid sequence of SEQ ID NO:7, or SEQ ID NO:8, or SEQ ID NO:9, or SEQ ID NO:10, or SEQ ID NO:11, or SEQ ID NO:12, or SEQ ID NO:13, or SEQ ID NO:14, or SEQ ID NO:15, or SEQ ID NO:16, or SEQ ID NO:17, or SEQ ID NO:18, or SEQ ID NO:19, or SEQ ID NO:20, or SEQ ID NO:21, or SEQ ID NO:22, or SEQ ID

NO:23, or SEQ ID NO:24, or SEQ ID NO:25, or SEQ ID NO:26, or SEQ ID NO:27, or SEQ ID NO:28, or SEQ ID NO:29, or SEQ ID NO:30, or SEQ ID NO: or SEQ ID NO:31, or SEQ ID NO:32, or SEQ ID NO:33, or SEQ ID NO:34, or SEQ ID NO:35, or SEQ ID NO:36, or SEQ ID NO:37, or SEQ ID NO:38, or SEQ ID NO: or SEQ ID NO:39, or SEQ ID NO:40, or SEQ ID NO:41, or SEQ ID NO:42.

The present invention further provides a method for identifying a protein having a bromodomain. One such embodiment comprises contacting a cellular extract with a peptide comprising an acetyl-lysine.

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The present invention further provides agents that can inhibit the binding of a bromodomain with a protein comprising an acetyl-lysine. In one embodiment the agent is ISYGR-AcK-KRRQRR (SEQ ID NO:4). In another embodiment the agent is ARKSTGG-AcK-APRKQL (SEQ ID NO:5). In still another embodiment the agent is QSTSRHK-AcK-LMFKTE (SEQ ID NO:6). In yet another embodiment the agent is an analog of acetyl-lysine such as acetyl-histamine. In still another embodiment the agent is an antibody that recognizes an acetyl-lysine of a protein binding partner of a bromodomain. In a preferred embodiment the agent is an antibody raised against a ZA loop of a bromodomain. These agents can be used as pharmaceuticals in compositions that contain a pharmaceutically acceptable carrier for example, or in the various drug assays of the present invention, serving as controls to demonstrate specificity.

Accordingly, it is a principal object of the present invention to provide the threedimensional coordinates of a bromodomain.

It is a further object of the present invention to provide the three-dimensional coordinates of a bromodomain complexed with acetyl-histamine.

It is a further object of the present invention to provide an assay for identifying proteins that contain bromodomains that bind proteins that comprise acetyl-lysine.

It is a further object of the present invention to provide methods of identifying drugs that can modulate the bromodomain-acetyl-lysine binding complex.

It is a further object of the present invention to provide methods of identifying drugs that can inhibit the binding of a bromodomain to a protein containing acetyl-lysine.

It is a further object of the present invention to provide methods that incorporate the use of rational design for identifying such drugs.

10 It is a further object of the present invention to provide a method of identifying drugs that can treat leukemia.

It is a further object of the present invention to provide a method of identifying drugs that can treat and/or prevent AIDS.

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These and other aspects of the present invention will be better appreciated by reference to the following drawings and Detailed Description.

BRIEF DESCRIPTION OF THE DRAWINGS

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Figure 1. Structure-based sequence alignment of a selected number of bromodomains. The sequences were aligned based on the NMR-derived structure of the P/CAF bromodomain, and the predicated four α-helices are shown in green boxes.

Bromodomains are grouped on the basis of the sequence and/or functional similarities as described by Jeanmougin *et al.*, [Trends in Biochemical *Sciences*, 22:151-153 (1997)]. Residue numbers of the P/CAF bromodomain are indicated above its sequence. Three absolutely conserved residues, corresponding to Pro751, Pro767, and Asn803 in the P/CAF bromodomain, are shown in red. Highly conserved residues are colored in blue. The residues of the P/CAF bromodomain that interact with acetyl-histamine, as determined by intermolecular NOEs, are indicated by asterisks. The ZA loop, which is critical for acetyl-lysine binding, for each of the indicated bromodomains is also identified. The underlined residues were changed individually

by site-directed mutagenesis to Ala. Genbank accession numbers for the proteins are as indicated in Table 8, in the Example below, along with the SEQ ID NOs. for the bromodomain sequences.

- Figures 2A-2H depict the structure of the P/CAF bromodomain. Figures 2A-2B shows the stereoview of the C_{α} trace of 30 superimposed NMR-derived structures of the bromodomain (residues 722-830). The N-terminal four residues (SKEP) which are structurally disordered are omitted for clarity. For the final 30 structures, the root-mean-square deviations (RMSDs) of the backbone and all heavy atoms are 0.63 10 \pm 0.11Å and 1.15 \pm 0.12Å for residues 723-830, respectively. The RMSDs of the backbone and all heavy atoms for the four α -helices (residues 727-743, 770-776, 785-802, and 807-827), are 0.34 ± 0.04 Å and 0.87 ± 0.06 Å, respectively. Figures 2C-2D show the stereoview of the bromodomain structures from the bottom of the protein, which is rotated approximately 90° from the orientation in Figures 2A-2B. Figure 2E shows the Ribbons [Carson, M., J. Appl. Crystallogr. 24:958-961 (1991)] 15 depiction of the averaged minimized NMR structure of the P/CAF bromodomain. The orientation of Figure 2E is as shown in Figures 2A-2B. Figures 2F-2G are schematic representations of the overall topology of the up-and-down four-helix bundle folds with the opposite handedness. The left-handed fold is seen in 20 bromodomain, cytochrome b_5 , and T4 lysozyme (left, Figure 2F), whereas the right-handed four-helix bundles are observed in proteins such as hemerythrin and cytochrome b₅₆₂ (right, Figure 2G) [Richardson, J., Adv. Protein Chem., 34:167-339 (1989); Presnell and Cohen, Proc. Natl. Acad. Sci. USA 86:6592-6596 (1989)]. Figure 2H is a molecular surface representation of the electrostatic potential (blue = positive; red = negative) of the bromodomain calculated in GRASP [Nicholls et al., 25 Biophys. J. 64:166-170 (1993)]. The hydrophobic and aromatic residues (Tyr809, Tyr802, Tyr760, Ala757, and Val752) located between the ZA and BC loops are
- 30 Figures 3A-3C show the binding of the P/CAF bromodomain to AcK. Figure 3A shows the superimposed region of the 2D ¹⁵N-HSQC spectra of the bromodomain (approximately 0.5 mM) in its free form (red) and complexed to the AcK-containing

indicated.

H4 peptide (molar ratio 1:6) (black). Figure 3B is the Ribbon and dotted-surface diagram of the bromodomain depicting the location of the lysine-acetylated H4 peptide binding site. The color coding reflects the chemical shift changes ($\Delta \delta$) of the backbone amide ¹H and ¹⁵N resonances upon binding to the AcK peptide as observed in the ¹⁵N-HSQC spectra. The normalized weighted average of the chemical shift changes was calculated by $\Delta_a / \Delta_{max} = [\Delta \delta_{NH} + \Delta \delta_N / 25)/2]^{1/2} / \Delta_{max}$, where Δ_{max} is the maximum weighted chemical shift difference observed for Tyr809 (0.16ppm). The backbone atoms are color-coded in red, yellow, or green for residues that have Δ_a / Δ_{max} of >0.6 (Tyr809, Glu808, Asn803, and Ala757), 0.2-0.6 (Ala813, Tyr802, Tyr760, and Val752), or <0.2 (Cys812, Ser807, Cys799, Phe796, and Phe748), respectively. The non-perturbed residues are shown in blue. Figure 3C shows the chemical structures of acetyl-lysine, acetyl-histamine, and acetyl-histidine.

Figure 4 depicts the acetyl-lysine binding pocket. This is the Ribbons [Carson, M., J. Appl. Crystallogr. 24:958-961 (1991)] depiction of a portion of the P/CAF bromodomain complexed with the acetyl-histamine. The ligand is color-coded by atom type.

DETAILED DESCRIPTION OF THE INVENTION

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The present invention identifies a general binding partner (ligand) for the protein motif known as the bromodomain. Indeed, by combining structural and site-directed mutagenesis studies the present invention demonstrates that bromodomains can interact specifically with acetyl-lysine (AcK), making them the first protein modules known to exhibit such interactions. Like other modular domains, such as Src homology-2 (SH2) and phosphotyrosine binding (PTB) domains, which specifically interact with phosphotyrosine-containing proteins, the bromodomain/acetyl-lysine recognition provides a means to regulate protein-protein interactions via protein lysine acetylation. The nature of the acetyl-lysine recognition by the bromodomain is similar to that of histone acetyltransferase interaction with acetyl-CoA. The present invention therefore couples for the first time, the functionality of the bromodomain with the HAT activity of coactivators in the regulation of gene transcription.

The present invention further provides both a nuclear magnetic resonance (NMR) structure of the bromodomain from the HAT coactivator P/CAF (p300/CBP-associated factor) as well as the structure for the P/CAF bromodomain in complex with acetyl-histamine. The structure reveals an unusual left-handed up-and-down four-helix bundle.

The results disclosed herein explain prior deletion experiments which showed that the bromodomain is indispensable for the function of GCN5 in yeast.

Bromodomain-AcK binding also appears to be important for the assembly and activity of multiprotein complexes in transcriptional activation. The results reported herein therefore, form the foundation for identifying specific biological ligands and for defining the molecular mechanisms by which the extensive family of bromodomains participate in chromatin remodeling and transcriptional activation

As disclosed herein, the binding partner for the bromodomain is a peptide or protein comprising an acetyl-lysine (AcK). Interestingly, whereas a free acetyl-lysine does not appear to bind the bromodomain, an analog of the acetyl-lysine, acetyl-histamine, does. This is most likely due to the additional charge present in the free amino acid. Consistently, free acetyl-histidine also does not to bind the bromodomain.

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The present invention further provides a key region of the bromodomain for the interaction with its acetyl-lysine binding partner, the ZA loop. The amino acid sequence of the ZA loop is defined in Figure 1 for a number of bromodomains and is depicted in Figure 2A for P/CAF. In a particular embodiment, the ZA loop has between about 21 and 40 amino acid residues comprising the amino acid sequence of:

$$F X_{2-3} P X_{5-8} J_{P/K/H} X Y J_{Y/F/H} X_5 P J_{M/I/V} D$$
 (SEQ ID NO:3)

more preferably the ZA loop has about 23 to 34 amino acid residues and comprises the amino acid sequence:

$$X_2 F X_{2-3} P X_{5-8} J_{P/K/H} X Y J_{Y/F/H} X_5 P J_{M/I/V} D$$
 (SEQ ID NO:43)

- (1) The single letter amino acid code is used in this description, *i.e.*, "F" for phenylalanine; "P" for proline; "Y" for tyrosine; and "D" for aspartic acid.
- (2) "X" indicates any amino acid (an undesignated amino acid); and X, X_2 , X_{2-3} , X_5 , and X_{5-8} indicates one undesignated amino acid, two consecutive undesignated amino acids, two or three consecutive undesignated amino acids, five consecutive undesignated amino acids, and five to eight consecutive undesignated amino acids respectively.
- (3) "J" indicates that identity of the amino acid is restricted to a particular group, again the one letter code is used
 - (i) $J_{P/K/H}$ is either proline, lysine or histidine.
 - (ii) $J_{Y/F/H}$ is either tyrosine, phenylalanine or histidine.
 - (iii) $J_{M/I/V}$ is either methionine, isoleucine, or valine.

Since this region of the bromodomain is important in binding its acetyl-lysine binding partner, antibodies specifically raised against this region are also included in the present invention. In a particular embodiment, the antibody is a humanized chimeric antibody that can be used in therapeutic treatment. Thus monoclonal, chimeric, and polyclonal antibodies raised against bromodomains, preferably against amino acid residues in the ZA loop region are part of the present invention. In a specific embodiment the antibody is raised against a peptide, fusion peptide or conjugated peptide consisting of amino acid residues 746 to 765 of SEQ ID NO:2, *i.e.*, WPFMEPVKRTEAPGYYEVIR (SEQ ID NO:44). Such antibodies can be used in the treatment of leukemia for example. Alternatively, these antibodies can be used in drug discovery assays.

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Thus the present invention provides the first detailed structural information regarding a bromodomain and a bromodomain complexed with its acetylated binding partner. The present invention therefore provides the three-dimensional structure of the bromodomain and a bromodomain acetylated binding partner complex. Since the interaction of the bromodomain with a histone for example, can play a significant role in chromatin remodeling/regulation, the structural information provided herein can be employed in methods of identifying drugs that can modulate basic cell processes by modulating the transcription. In a particular embodiment, the three-dimensional

structural information is used in the design of a small organic molecule for the treatment of cancer.

Indeed, the bromodomain and lysine-acetylated protein interaction can now be implicated to play a causal role in the development of a number of diseases including cancers such as leukemia. For example, chromatin remodeling plays a central role in the etiology of viral infection and cancer [Archer and Hodin, Curr. Opin. Genet. Biol. 9:171-174 (1999); Jacobson and Pillus, Curr. Opin. Genet. Biol. 9:175-184 (1999)]. Both altered histone acetylation/deacetylation and aberrant forms of chromatin-10 remodeling complexes are associated with human diseases. Furthermore, chromosomal translocation of various cellular genes with those encoding HATs and subunits of chromatin remodeling complexes have been implicated in leukomogenesis. The MOZ (monocytic leukemia zinc finger) and MLL/ALL-1 genes are frequently fused to the gene encoding the co-activator HAT CBP [Sobulo et al., Proc. Natl. Acad. Sci. 15 USA 94:8732-8737(1997)]. The resulting fusion protein MLL-CBP contains the tandem bromodomain-PHD finger-HAT domain of CBP. It also has been shown that both the bromodomain and HAT domain of CBP are required for leukomogenesis, because deletion of either the bromodomain or the HAT domain results in loss of the MLL-CBP fusion protein's ability for cell transform. These results indicate that the 20 CBP bromodomain, and more particularly, the ZA loop of the CBP bromodomain, is an excellent target for developing drugs that interfere with the bromodomain acetyllysine interaction that can be used in the treatment of human acute leukemia. In addition, an antibody (e.g., a humanized antibody) raised specifically against a peptide from the ZA loop of the CBP bromodomain could also be effective for treating these 25 conditions.

Furthermore, the human immunodeficiency virus type 1 (HIV-1) trans-activator protein, Tat, is absolutely required for productive HIV viral replication [Jeang and Gatignol, Curr. Top. Microbiol. Immunol., 188:123-144(1994)]. Recently, it has been shown that HIV-1 Tat transcriptional activity is tightly regulated by lysine acetylation [Kiernan et al., EMBO Journal 18:6106-6118 (1999)]. Therefore, the interaction of the acetyl-lysine of Tat with one or more bromodomain-containing proteins associated

with chromatin remodeling could mediate gene transcription. Thus, the bromodomain/lysine-acetylated Tat interaction could also serve as a drug target for blocking HIV replication in cells. Similarly, an antibody raised specifically against a peptide from the ZA loop of the bromodomain could also be effective for treating these conditions.

In addition, based on the new structural information disclosed herein, the key amino acid residues for the binding of a given bromodomain and its binding partner can be identified and further elucidated using basic mutagenesis and standard isothermal titration calorimetry, for example. In this case, both the crucial amino acids for the bromodomain and the binding partner (i.e., apart from the acetyl-lysine) can be readily determined and are also part of the present invention.

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The results obtained from the structural and functional studies disclosed herein provide
the foundation for both high throughput drug screening and structure-based rational
drug design. The agents identified by this procedure will be useful for ameliorating
conditions involving chromatin remodeling/regulation as indicated above.

Structure based rational drug design is the most efficient method of drug development.

However, heretofore, no information has been disclosed regarding the structure of the bromodomain or more importantly, its interaction with the acetyl-lysine of its binding partner. Obtaining detailed structural information requires an extensive NMR or X-ray crystallographic analysis. By determining and then exploiting the detailed structural information of the bromodomain and of the bromodomain/acetyl-histamine

(exemplified by NMR analysis below) the present invention provides novel methods for developing new drugs through structure based rational drug design.

Thus the present invention provides representative sets of the atomic structure coordinates of the free form of the P/CAF bromodomain (Table 5) and of the P/CAF bromodomain-acetyl-histamine complex (Table 6) which were both obtained by NMR analysis. A Ribbon diagram of the three-dimensional structure of the P/CAF bromodomain is depicted in Figure 2E, whereas the P/CAF bromodomain acetyl-lysine

binding pocket is depicted in Figure 4. The present invention also provides the NOE-derived distance restraints, and NMR chemical shift assignments of the P/CAF bromodomain. The NMR chemical shift assignments of the P/CAF bromodomain are included in the chemical shift table (Table 1) for the ¹H-¹⁵N HSQC spectrum of P/CAF bromodomain. The unambiguous NOE-derived Inter-proton Distance Restraints (Table 2), the ambiguous NOE-derived Inter-proton Distance Restraints (Table 3) and the ¹H bonding restraints (Table 4) are also disclosed herein. The sample atomic coordinate data provided enable the skilled artisan to practice the invention. In addition, Tables 1-6 are also capable of being placed into a computer readable form which is also part of the present invention. Furthermore, methods of using these coordinates and chemical shifts and related information (including in computer readable forms) either individually or together in drug assays are also provided. More particularly, such atomic coordinates can be used to identify potential ligands or drugs which will modulate the binding of a bromodomain with its binding partner.

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Therefore, if appearing herein, the following terms shall have the definitions set out below.

As used herein a "bromodomain-acetyl-lysine binding complex" is a binding complex between a bromodomain or fragment thereof and either a peptide/polypeptide comprising an acetyl-lysine (or an analog of acetyl-lysine), or a free analog of acetyl-lysine, such as acetyl-histamine disclosed in the Example below. Preferably, the peptide comprises at least six amino acids in addition to the acetyl-lysine. The dissociation constant of a bromodomain-acetyl-lysine binding complex is dependent on whether the lysine residue or analog thereof is acetylated or not, such that the affinity for the bromodomain and the peptide comprising the lysine residue (for example) significantly decreases when that lysine residue is not acetylated.

As used herein a "ZA loop" of a bromodomain is one protion of a bromodomain that is involved in the binding of the bromodomain to the acetyl-lysine. The structure of the ZA loop of the bromodomain of for P/CAF is depicted in Figure 2A. The ZA loop has between about 20 and 40 amino acids and comprises the amino acid sequence of SEQ ID NO:3. More preferably the ZA loop comprises between about 23 to 34 amino acids

and has the amino acid sequence SEQ ID NO:43. The amino acid sequence of the ZA loop for a representative number of individual bromodomains is shown in Figure 1.

A "polypeptide" or "peptide" comprising a fragment of a bromodomain, such as the ZA loop, or a peptide or polypeptide comprising an acetyl-lysine, as used herein can be the "fragment" alone, or a larger chimeric or fusion peptide/protein which contains the "fragment".

As used herein the terms "fusion protein" and "fusion peptide" are used interchangeably and encompass "chimeric proteins and/or chimeric peptides" and fusion "intein proteins/peptides". A fusion protein comprises at least a portion of a protein or peptide of the present invention, e.g., a bromodomain, joined via a peptide bond to at least a portion of another protein or peptide including e.g., a second bromodomain in a chimeric fusion protein. In a particular embodiment the portion of the bromodomain is antigenic. Fusion proteins can comprise a marker protein or peptide, or a protein or peptide that aids in the isolation and/or purification of the protein, for example.

As used herein, and unless otherwise specified, the terms "agent", "potential drug", "compound", "test compound" or "potential compound" are used interchangeably, and refer to chemicals which potentially have a use as an inhibitor or activator/stabilizer of bromodomain-acetyl-lysine binding. Therefore, such "agents", "potential drugs", "compounds" and "potential compounds" may be used, as described herein, in drug assays and drug screens and the like.

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As used herein a "small organic molecule" is an organic compound, including a peptide [or organic compound complexed with an inorganic compound (e.g., metal)] that has a molecular weight of less than 3 Kilodaltons. Such small organic molecules can be included as agents, etc. as defined above.

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As used herein the term "binds to" is meant to include all such specific interactions that result in two or more molecules showing a preference for one another relative to some third molecule. This includes processes such as covalent, ionic, hydrophobic and

hydrogen bonding but does not include non-specific associations such as solvent preferences.

As used herein the term "about" signifies that a value is within twenty percent of the indicated value *i.e.*, a peptide containing "about" 20 amino acid residues can contain between 16 and 24 amino acid residues.

General Techniques for Constructing Nucleic Acids That Encode the Bromodomains and Fragments Thereof (Incuding, ZA Loops); and the Bromodomain Binding Partners of the Present Invention.

In accordance with the present invention there may be employed conventional molecular biology, microbiology, and recombinant DNA techniques within the skill of the art. Such techniques are explained fully in the literature. See, e.g., Sambrook,

- Fritsch & Maniatis, Molecular Cloning: A Laboratory Manual, Second Edition (1989)
 Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York (herein "Sambrook et al., 1989"); DNA Cloning: A Practical Approach, Volumes I and II
 (D.N. Glover ed. 1985); Oligonucleotide Synthesis (M.J. Gait ed. 1984); Nucleic Acid Hybridization [B.D. Hames & S.J. Higgins eds. (1985)]; Transcription And
- 20 Translation [B.D. Hames & S.J. Higgins, eds. (1984)]; Animal Cell Culture [R.I. Freshney, ed. (1986)]; Immobilized Cells And Enzymes [IRL Press, (1986)]; B. Perbal, A Practical Guide To Molecular Cloning (1984); F.M. Ausubel et al. (eds.), Current Protocols in Molecular Biology, John Wiley & Sons, Inc. (1994).
- Therefore, if appearing herein, the following terms shall have the definitions set out below.

As used herein, the term "gene" refers to an assembly of nucleotides that encode a polypeptide, and includes cDNA and genomic DNA nucleic acids.

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A "vector" is a replicon, such as plasmid, phage or cosmid, to which another DNA segment may be attached so as to bring about the replication of the attached segment. A "replicon" is any genetic element (e.g., plasmid, chromosome, virus) that functions

as an autonomous unit of DNA replication *in vivo*, *i.e.*, capable of replication under its own control.

A "cassette" refers to a segment of DNA that can be inserted into a vector at specific restriction sites. The segment of DNA encodes a polypeptide of interest, and the cassette and restriction sites are designed to ensure insertion of the cassette in the proper reading frame for transcription and translation.

A cell has been "transfected" by exogenous or heterologous DNA when such DNA has been introduced inside the cell.

A "nucleic acid molecule" refers to the phosphate ester polymeric form of ribonucleosides (adenosine, guanosine, uridine or cytidine; "RNA molecules") or deoxyribonucleosides (deoxyadenosine, deoxyguanosine, deoxythymidine, or deoxycytidine; "DNA molecules"), or any phosphoester analogues thereof, such as phosphorothioates and thioesters, in either single stranded form, or a double-stranded helix. Double stranded DNA-DNA, DNA-RNA and RNA-RNA helices are possible. The term nucleic acid molecule, and in particular DNA or RNA molecule, refers only to the primary and secondary structure of the molecule, and does not limit it to any 20 particular tertiary forms. Thus, this term includes double-stranded DNA found, inter alia, in linear or circular DNA molecules (e.g., restriction fragments), plasmids, and chromosomes. In discussing the structure of particular double-stranded DNA molecules, sequences may be described herein according to the normal convention of giving only the sequence in the 5' to 3' direction along the nontranscribed strand of 25 DNA (i.e., the strand having a sequence homologous to the mRNA). A "recombinant DNA molecule" is a DNA molecule that has undergone a molecular biological manipulation.

A nucleic acid molecule is "hybridizable" to another nucleic acid molecule, such as a cDNA, genomic DNA, or RNA, when a single stranded form of the nucleic acid molecule can anneal to the other nucleic acid molecule under the appropriate conditions of temperature and solution ionic strength (see Sambrook et al., supra). The conditions of temperature and ionic strength determine the "stringency" of the

hybridization. For preliminary screening for homologous nucleic acids, low stringency hybridization conditions, corresponding to a T_m of 55°, can be used, e.g., 5x SSC, 0.1% SDS, 0.25% milk, and no formamide; or 30% formamide, 5x SSC, 0.5% SDS). Moderate stringency hybridization conditions correspond to a higher T_m, e.g., 40% formamide, with 5x or 6x SCC. High stringency hybridization conditions correspond to the highest T_m, e.g., 50% formamide, 5x or 6x SCC. Hybridization requires that the two nucleic acids contain complementary sequences, although depending on the stringency of the hybridization, mismatches between bases are possible. The appropriate stringency for hybridizing nucleic acids depends on the length of the 10 nucleic acids and the degree of complementation, variables well known in the art. The greater the degree of similarity or homology between two nucleotide sequences, the greater the value of T_m for hybrids of nucleic acids having those sequences. The relative stability (corresponding to higher T_m) of nucleic acid hybridizations decreases in the following order: RNA:RNA, DNA:RNA, DNA:DNA. For hybrids of greater than 100 nucleotides in length, equations for calculating T_m have been derived (see Sambrook et al., supra, 9.50-10.51). For hybridization with shorter nucleic acids, i.e., oligonucleotides, the position of mismatches becomes more important, and the length of the oligonucleotide determines its specificity (see Sambrook et al., supra, 11.7-11.8). Preferably a minimum length for a hybridizable nucleic acid is at least about 12 nucleotides; preferably at least about 18 nucleotides; and more preferably the length is 20 at least about 27 nucleotides; and most preferably 36 nucleotides.

In a specific embodiment, the term "standard hybridization conditions" refers to a T_m of 55°C, and utilizes conditions as set forth above. In a preferred embodiment, the T_m is 60°C; in a more preferred embodiment, the T_m is 65°C.

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A DNA "coding sequence" is a double-stranded DNA sequence which is transcribed and translated into a polypeptide in a cell *in vitro* or *in vivo* when placed under the control of appropriate regulatory sequences. The boundaries of the coding sequence are determined by a start codon at the 5' (amino) terminus and a translation stop codon at the 3' (carboxyl) terminus. A coding sequence can include, but is not limited to, prokaryotic sequences and synthetic DNA sequences. If the coding sequence is

intended for expression in a eukaryotic cell, a polyadenylation signal and transcription termination sequence will usually be located 3' to the coding sequence.

Transcriptional and translational control sequences are DNA regulatory sequences, such as promoters, enhancers, terminators, and the like, that provide for the expression of a coding sequence in a host cell. In eukaryotic cells, polyadenylation signals are control sequences.

A "promoter sequence" is a DNA regulatory region capable of binding RNA

10 polymerase in a cell and initiating transcription of a downstream (3' direction) coding sequence. For purposes of defining the present invention, the promoter sequence is bounded at its 3' terminus by the transcription initiation site and extends upstream (5' direction) to include the minimum number of bases or elements necessary to initiate transcription at levels detectable above background. Within the promoter sequence

15 will be found a transcription initiation site (conveniently defined for example, by mapping with nuclease S1), as well as protein binding domains (consensus sequences) responsible for the binding of RNA polymerase.

A coding sequence is "under the control" of transcriptional and translational control sequences in a cell when RNA polymerase transcribes the coding sequence into mRNA, which is then trans-RNA spliced and translated into the protein encoded by the coding sequence.

A DNA sequence is "operatively linked" to an expression control sequence when the
expression control sequence controls and regulates the transcription and translation of
that DNA sequence. The term "operatively linked" includes having an appropriate
start signal (e.g., ATG) in front of the DNA sequence to be expressed and maintaining
the correct reading frame to permit expression of the DNA sequence under the control
of the expression control sequence and production of the desired product encoded by
the DNA sequence. If a gene that one desires to insert into a recombinant DNA
molecule does not contain an appropriate start signal, such a start signal can be inserted
in front of the gene.

As used herein, the term "homologous" in all its grammatical forms refers to the relationship between proteins that possess a "common evolutionary origin," including proteins from superfamilies (e.g., the immunoglobulin superfamily) and homologous proteins from different species (e.g., myosin light chain, etc.) [Reeck et al., Cell, 50:667 (1987)]. Such proteins have sequence homology as reflected by their high degree of sequence similarity.

Accordingly, the term "sequence similarity" in all its grammatical forms refers to the degree of identity or correspondence between nucleic acid or amino acid sequences of proteins that may or may not share a common evolutionary origin (see Reeck et al., supra). However, in common usage and in the instant application, the term "homologous," when modified with an adverb such as "highly," may refer to sequence similarity and not a common evolutionary origin.

15 Two DNA sequences are "substantially homologous" when at least about 60% (preferably at least about 80%, and most preferably at least about 90 or 95%) of the nucleotides match over the defined length of the DNA sequences. Sequences that are substantially homologous can be identified by comparing the sequences using standard software available in sequence data banks, or in a Southern hybridization experiment under, for example, stringent conditions as defined for that particular system. Defining appropriate hybridization conditions is within the skill of the art. See, e.g., Maniatis et al., supra; DNA Cloning, Vols. I & II, supra; Nucleic Acid Hybridization, supra.

As used herein an amino acid sequence is 100% "homologous" to a second amino acid sequence if the two amino acid sequences are identical, and/or differ only by neutral or conservative substitutions as defined below. Accordingly, an amino acid sequence is 50% "homologous" to a second amino acid sequence if 50% of the two amino acid sequences are identical, and/or differ only by neutral or conservative substitutions.

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As used herein, DNA and protein sequence percent identity can be determined using MacVector 6.0.1, Oxford Molecular Group PLC (1996) and the Clustal W algorithm with the alignment default parameters, and default parameters for identity. These

commercially available programs can also be used to determine sequence similarity using the same or analogous default parameters.

The term "corresponding to" is used herein to refer similar or homologous sequences, whether the exact position is identical or different from the molecule to which the similarity or homology is measured. Thus, the term "corresponding to" refers to the sequence similarity, and not the numbering of the amino acid residues or nucleotide bases.

As used herein a "heterologous nucleotide sequence" is a nucleotide sequence that is added to a nucleotide sequence of the present invention by recombinant methods to form a nucleic acid which is not naturally formed in nature. Such nucleic acids can encode fusion proteins or peptides, including chimeric proteins and peptides. Thus the heterologous nucleotide sequence can encode peptides and/or proteins which contain regulatory and/or structural properties. In another such embodiment the heterologous nucleotide can encode a protein or peptide that functions as a means of detecting the protein or peptide encoded by the nucleotide sequence of the present invention after the recombinant nucleic acid is expressed. In still another such embodiment the heterologous nucleotide can function as a means of detecting a nucleotide sequence of the present invention. A heterologous nucleotide sequence can comprise non-coding sequences including restriction sites, regulatory sites, promoters and the like.

The present invention also relates to cloning vectors containing nucleic acids encoding analogs and derivatives of the bromodomains of the present invention and polypeptides/peptides that can bind a bromodomain when a lysine of the polypeptide/peptide is acetylated, including modified fragments, that have the same or homologous functional activity as the individual fragments, and homologs thereof. The production and use of derivatives and analogs related to the fragments are within the scope of the present invention.

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Due to the degeneracy of nucleotide coding sequences, other DNA sequences which encode substantially the same amino acid sequence as a nucleic acid encoding a protein

comprising bromodomain or bromodomain binding partner (i.e., when posttranscriptionally acetylated) of the present invention for example, may be used in the practice of the present invention. These include but are not limited to allelic genes, homologous genes from other species, which are altered by the substitution of different codons that encode the same amino acid residue within the sequence, thus producing a silent change. Likewise, the peptides and polypeptides of the present invention include, but are not limited to, those containing, as a primary amino acid sequence, analogous portions of their respective amino acid sequences including altered sequences in which functionally equivalent amino acid residues are substituted for 10 residues within the sequence resulting in a conservative amino acid substitution. For example, one or more amino acid residues within the sequence can be substituted by another amino acid of a similar polarity, which acts as a functional equivalent, resulting in a silent alteration. Substitutes for an amino acid within the sequence may be selected from other members of the class to which the amino acid belongs. For example, the nonpolar (hydrophobic) amino acids include alanine, leucine, isoleucine, 15 valine, proline, phenylalanine, tryptophan and methionine. Amino acids containing aromatic ring structures are phenylalanine, tryptophan, and tyrosine. The polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine. The positively charged (basic) amino acids include arginine, and lysine. 20 The negatively charged (acidic) amino acids include aspartic acid and glutamic acid.

Particularly preferred conserved amino acid exchanges are:

- (a) Lys for Arg or vice versa such that a positive charge may be maintained;
- (b) Glu for Asp or vice versa such that a negative charge may be maintained;
- 25 (c) Ser for Thr or vice versa such that a free -OH can be maintained;
 - (d) Gln for Asn or vice versa such that a free NH₂ can be maintained;
 - (e) Ile for Leu or for Val or vice versa as roughly equivalent hydrophobic amino acids; and
 - (f) Phe for Tyr or vice versa as roughly equivalent aromatic amino acids.

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A conservative change generally leads to less change in the structure and function of the resulting protein. A non-conservative change is more likely to alter the structure, activity or function of the resulting protein. The present invention should be considered to include sequences containing conservative changes which do not significantly alter the activity or binding characteristics of the resulting protein. Specific amino acid residues for the P/CAF bromodomain have been identified that are important for binding, indicating a potential lower stringency for the substitution of the remaining amino acids residues.

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All of the peptides/fragments of the present invention can be modified by being placed in a fusion or chimeric peptide or protein, or labeled e.g., to have an N-terminal FLAG10 tag, or H6 tag. In a particular embodiment the P/CAF bromodomain fragment can be modified to contain a marker protein such as green fluorescent protein as described in U.S. Patent No. 5,625,048 filed April 29, 1997 and WO 97/26333, published July 24, 1997 each of which are hereby incorporated by reference herein in their entireties.

- The nucleic acids encoding peptides and protein fragments of the present invention and 15 analogs thereof can be produced by various methods known in the art. The manipulations which result in their production can occur at the gene or protein level [Sambrook et al., 1989, supra]. The nucleotide sequence can be cleaved at appropriate sites with restriction endonuclease(s), followed by further enzymatic modification if 20 desired, isolated, and ligated in vitro. In addition a nucleic acid sequence can be mutated in vitro or in vivo, to create and/or destroy translation, initiation, and/or termination sequences, or to create variations in coding regions and/or form new restriction endonuclease sites or destroy preexisting ones, to facilitate further in vitro modification. Any technique for mutagenesis known in the art can be used, including 25 but not limited to, in vitro site-directed mutagenesis [Hutchinson et al., J. Biol. Chem., 253:6551 (1978); Zoller and Smith, DNA, 3:479-488 (1984); Oliphant et al., Gene, 44:177 (1986); Hutchinson et al., Proc. Natl. Acad. Sci. U.S.A., 83:710 (1986)], use of TAB® linkers (Pharmacia), etc. PCR techniques are preferred for site directed mutagenesis [see Higuchi, 1989, "Using PCR to Engineer DNA", in PCR Technology: Principles and Applications for DNA Amplification, H. Erlich, ed., Stockton Press,
- Chapter 6, pp. 61-70].

The identified and isolated nucleic acids can then be inserted into an appropriate cloning vector. A large number of vector-host systems known in the art may be used.

Protein expression and purification

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A bacterial protein expression system can be used to make various stable isotopically labeled (¹³C, ¹⁵N, and ²H) protein samples that are useful for a three-dimensional NMR structural determination of a protein complex. For example a pET14b (Novagen) bacterial expression vector can be constructed which expresses the recombinant P/CAF bromodomain as an amino-terminal His-tagged fusion protein.

Protein expression and purification can be conducted using standard procedures for His-tagged proteins [Zhou et al., J. Biol. Chem. 270:31119-31123 (1995)]. To optimize the level of protein expression, various bacterial growth and expression conditions can be screened, which include different E. Coli cell lines, and growth and protein induction temperatures. Generally, it is preferred to obtain the maximum amount of soluble protein while still inducing protein expression with a relatively low IPTG concentration e.g., ~0.2mM (final concentration) at 16°C. As exemplified below, the bromodomain of P/CAF (residues 719-832 of SEQ ID NO:2 which is SEQ ID NO:7) was subcloned into the pET14b expression vector (Novagen) and expressed in Escherichia coli BL21(DE3) cells. Uniformly ¹⁵N- and ¹⁵N/¹³C-labeled proteins were prepared by growing bacteria in a minimal medium containing ¹⁵NH₄Cl with or without ¹³C₆-glucose. A uniformly ¹⁵N/¹³C-labeled and fractionally deuterated protein sample was prepared by growing the cells in 75% ²H₂O. The bromodomain was purified by affinity chromatography on a nickel-IDA column (Invitrogen) followed by the removal of poly-His tag by thrombin cleavage. The final purification of the protein was achieved by size-exclusion chromatography. The acetyl-lysine-containing peptides were prepared on a MilliGen 9050 peptide synthesizer (Perkin Elmer) using Fmoc/HBTU chemistry. Acetyl-lysine was incorporated using the reagent Fmoc-Ac-Lys with HBTU/DIPEA activation. NMR samples contained approximately 1 mM protein in 100mM phosphate buffer of pH 6.5 and 5mM perdeuterated DTT and

0.5mM EDTA in $H_2O/^2H_2O$ (9/1) or 2H_2O .

One major advantage of using the heteronuclear multidimensional approach, as exemplied herein, is that the NMR resonance assignments of a protein are obtained in a sequence-specific manner which assures accuracy and greatly facilitates data analysis and structure determination [Clore, G. M. & Gronenborn, A. M. Meth. Enzymol.

- 239:249-363 (1994)]. In addition, the signal overlapping problems in the protein spectra are minimized by the use of multidimensional NMR spectra, which separates the proton signals according to the chemical shifts of their attached hetero-nuclei (such as ¹⁵N and ¹³C). This NMR approach has been proven very powerful for structural analysis of large proteins [Clore, G. M. & Gronenborn, A. M. Meth. Enzymol.
- 239:249-363 (1994)]. To facilitate sequence-specific resonance assignments for the structural study, a uniformly ¹³C, ¹⁵N-labeled and fractionally (75%) deuterated protein sample of the bromodomain can be prepared by growing bacterial cells in 75% ²H₂O as exemplified below. Such protein samples can be used for triple-resonance NMR experiments. A triple-labeled protein sample is useful for high-resolution NMR structural studies. Because of the favorable ¹H, ¹³C, and ¹⁵N relaxation rates caused by
 - the partial deuteration of the protein, constant-time triple-resonance NMR spectra can be acquired with higher digital resolution and sensitivity [Sattler, M. & Fesik, S. W. *Structure* 4:1245-1249 (1996)]. In addition, various stable-isotopically labeled (¹⁵N and ¹³C /¹⁵N) proteins can also be prepared using this procedure.

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Synthetic Polypeptides

The term "polypeptide" is used in its broadest sense to refer to a compound of two or more subunit amino acids, amino acid analogs, or peptidomimetics. The subunits are linked by peptide bonds. The terms "polypeptide", "protein", and "peptide" are used interchangeably herein, though preferably as used herein a "peptide" refers to a compound of at least two but less than fifty subunit amino acids, and a polypeptide or protein refers to compound of fifty or more amino acids. The polypeptides of the present invention may be chemically synthesized or as detailed above, genetically engineered or isolated from natural sources.

In addition, potential drugs or agents that may be tested in the drug screening assays of the present invention may also be chemically synthesized. When the peptide is to be modified, e.g., acetylated, the modification can be at any time during the peptide synthesis, including using an acetyl-lysine as a starting material or acetylating a lysine residue of a peptide after the peptide has been synthesized. In the Example below, the acetyl-lysine-containing peptides were prepared on a MilliGen 9050 peptide synthesizer (Perkin Elmer) using Fmoc/HBTU chemistry. Acetyl-lysine was incorporated using the reagent Fmoc-Ac-Lys with HBTU/DIPEA activation.

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Thus, synthetic polypeptides, prepared using the well known techniques of solid phase, liquid phase, or peptide condensation techniques, or any combination thereof, can include natural and unnatural amino acids. Amino acids used for peptide synthesis may be standard Boc (N^{α} -amino protected N^{α} -t-butyloxycarbonyl) amino acid resin with the standard deprotecting, neutralization, coupling and wash protocols of the original solid phase procedure of Merrifield [J. Am. Chem. Soc., 85:2149-2154 (1963)], or the base-labile N^α-amino protected 9-fluorenylmethoxycarbonyl (Fmoc) amino acids first described by Carpino and Han [J. Org. Chem., 37:3403-3409 (1972)]. Both Fmoc and Boc N^α-amino protected amino acids can be obtained from Fluka, Bachem, Advanced Chemtech, Sigma, Cambridge Research Biochemical, Bachem, or Peninsula Labs or other chemical companies familiar to those who practice this art. In addition, the method of the invention can be used with other N°-protecting groups that 20 are familiar to those skilled in this art. Solid phase peptide synthesis may be accomplished by techniques familiar to those in the art and provided, for example, in Stewart and Young [Solid Phase Synthesis, Second Edition, Pierce Chemical Co., Rockford, IL (1984)] and Fields and Noble [Int. J. Pept. Protein Res., 35:161-214 (1990)], or using automated synthesizers, such as sold by ABS. Thus, polypeptides of the invention may comprise D-amino acids, a combination of D- and L-amino acids, 25 and various "designer" amino acids (e.g., β-methyl amino acids, Cα-methyl amino acids, and Nα-methyl amino acids, etc.) to convey special properties. Synthetic amino acids include ornithine for lysine, fluorophenylalanine for phenylalanine, and norleucine for leucine or isoleucine. Additionally, by assigning specific amino acids at specific coupling steps, α -helices, β turns, β sheets, γ -turns, and cyclic peptides can be 30 generated.

In a further embodiment, subunits of peptides that confer useful chemical and structural properties will be chosen. For example, peptides comprising D-amino acids will be resistant to L-amino acid-specific proteases in vivo. In addition, the present invention envisions preparing peptides that have more well defined structural properties, and the use of peptidomimetics, and peptidomimetic bonds, such as ester bonds, to prepare peptides with novel properties. In another embodiment, a peptide may be generated that incorporates a reduced peptide bond, i.e., R₁-CH₂-NH-R₂, where R_1 and R_2 are amino acid residues or sequences. A reduced peptide bond may be introduced as a dipeptide subunit. Such a molecule would be resistant to peptide bond hydrolysis, e.g., protease activity. Such peptides would provide ligands with unique function and activity, such as extended half-lives in vivo due to resistance to metabolic breakdown, or protease activity. Furthermore, it is well known that in certain systems constrained peptides show enhanced functional activity [Hruby, Life Sciences, 31:189-199 (1982); Hruby et al., Biochem J., 268:249-262 (1990)]; the present invention provides a method to produce a constrained peptide that incorporates random sequences at all other positions.

Constrained and cyclic peptides. A constrained, cyclic or rigidized peptide may be prepared synthetically, provided that in at least two positions in the sequence of the peptide an amino acid or amino acid analog is inserted that provides a chemical functional group capable of crosslinking to constrain, cyclise or rigidize the peptide after treatment to form the crosslink. Cyclization will be favored when a turn-inducing amino acid is incorporated. Examples of amino acids capable of crosslinking a peptide are cysteine to form disulfides, aspartic acid to form a lactone or a lactam, and a chelator such as γ-carboxyl-glutamic acid (Gla) (Bachem) to chelate a transition metal and form a cross-link. Protected γ-carboxyl glutamic acid may be prepared by modifying the synthesis described by Zee-Cheng and Olson [Biophys. Biochem. Res. Commun., 94:1128-1132 (1980)]. A peptide in which the peptide sequence comprises at least two amino acids capable of crosslinking may be treated, e.g., by oxidation of cysteine residues to form a disulfide or addition of a metal ion to form a chelate, so as to crosslink the peptide and form a constrained, cyclic or rigidized peptide.

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The present invention provides strategies to systematically prepare cross-links. For example, if four cysteine residues are incorporated in the peptide sequence, different protecting groups may be used (Hiskey, in The Peptides: Analysis, Synthesis, Biology, Vol. 3, Gross and Meienhofer, eds., Academic Press: New York, pp. 137-167 (1981);

Ponsanti et al., Tetrahedron, 46:8255-8266 (1990)]. The first pair of cysteines may be deprotected and oxidized, then the second set may be deprotected and oxidized. In this way a defined set of disulfide cross-links may be formed. Alternatively, a pair of cysteines and a pair of chelating amino acid analogs may be incorporated so that the cross-links are of a different chemical nature.

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Non-classical amino acids that induce conformational constraints. The following non-classical amino acids may be incorporated in the peptide in order to introduce particular conformational motifs: 1,2,3,4-tetrahydroisoquinoline-3-carboxylate [Kazmierski et al., J. Am. Chem. Soc., 113:2275-2283 (1991)]; (2S,3S)-methyl-

- phenylalanine, (2S,3R)-methyl-phenylalanine, (2R,3S)-methyl-phenylalanine and (2R,3R)-methyl-phenylalanine (Kazmierski and Hruby, *Tetrahedron Lett.* (1991)]; 2-aminotetrahydronaphthalene-2-carboxylic acid [Landis, Ph.D. Thesis, University of Arizona (1989)]; hydroxy-1,2,3,4-tetrahydroisoquinoline-3-carboxylate [Miyake *et al.*, *J. Takeda Res. Labs.*, **43**:53-76 (1989)]; β-carboline (D and L) [Kazmierski, Ph.D.
- Thesis, University of Arizona (1988)]; HIC (histidine isoquinoline carboxylic acid) [Zechel et al., Int. J. Pep. Protein Res., 43 (1991)]; and HIC (histidine cyclic urea) (Dharanipragada).

The following amino acid analogs and peptidomimetics may be incorporated into a

peptide to induce or favor specific secondary structures: LL-Acp (LL-3-amino2-propenidone-6-carboxylic acid), a β-turn inducing dipeptide analog [Kemp et al., J.

Org. Chem., 50:5834-5838 (1985)]; β-sheet inducing analogs [Kemp et al.,

Tetrahedron Lett., 29:5081-5082 (1988); β-turn inducing analogs [Kemp et al.,

Tetrahedron Lett., 29:5057-5060 (1988)]; α-helix inducing analogs (Kemp et al.,

Tetrahedron Lett., 29:4935-4938 (1988)]; γ-turn inducing analogs [Kemp et al., J.

Org. Chem., 54:109:115 (1989)]; and analogs provided by the following references:

Nagai and Sato, Tetrahedron Lett., 26:647-650 (1985); DiMaio et al., J. Chem. Soc.

Perkin Trans., p. 1687 (1989); also a Gly-Ala turn analog [Kahn et al., Tetrahedron

spectra of mutated proteins can be compared to that of the wild-type protein bromodomain.

Chemical-shift perturbations due to ligand binding have proven to be a reliable and sensitive probe for the ligand binding site of the protein. This is because the chemicalshift changes of the backbone amide groups are likely to reflect any changes in protein conformation and/or hydrogen bonding due to the peptide/ligand binding. To examine the effects of a mutation on the ligand binding (in this case the ligand is a peptide comprising an acetyl-lysine), peptide titration experiments can be conducted by following the changes of ¹H/¹⁵N signals of the mutant proteins as a function of the 10 peptide concentration. These experiments indicate whether the acetyl-lysine binding site remains the same or changes in the mutants relative to the wild type protein. The effects of the mutation on the peptide binding affinity can also be examined by NMR spectroscopy. If the mutated proteins result in the reduction of the binding affinity, a 15 change of the exchange phenomenon between the free and the ligand-bound signals should be observed in NMR spectrum. If the reduction in binding affinity causes the peptide binding to change from a slow exchange rate to a fast exchange rate, on the NMR time scale, then the peptide binding affinity can be determined from the NMR titration experiment. From these mutation analyses key amino acid residues that are important for binding a peptide comprising the acetyl-lysine can be identified. Such 20 analysis has been exemplified below.

Protein Structure Determination by NMR Spectroscopy

The NMR results from the present invention are summarized by the atomic structure coordinates of the free form of the P/CAF bromodomain (Table 5) and of the P/CAF bromodomain-acetyl-histamine complex (Table 6). The NMR chemical shift assignments of the P/CAF bromodomain are included in the chemical shift table (Table 1) for the ¹H-¹⁵N HSQC spectrum of P/CAF bromodomain. The unambiguous NOE-derived Inter-proton Distance Restraints are in Table 2, the ambiguous NOE-derived Inter-proton Distance Restraints are in Table 3, and the ¹H bonding restraints are disclosed in Table 4.

Backbone and Side-chain Assignments: Sequence-specific backbone assignment can be achieved by using a suite of deuterium-decoupled triple-resonance 3D NMR experiments which include HNCA, HN(CO)CA, HN(CA)CB, HN(COCA)CB, HNCO, and HN(CA)CO experiments [Yamazaki, et al., J. Am. Chem. Soc. 116:11655-11666
5 (1994)]. The water flip-back scheme is used in these NMR pulse programs to minimize amide signal attenuation from water exchange. Sequential side-chain assignments are typically accomplished from a series of 3D NMR experiments with alternative approaches to confirm the assignments. These experiments include 3D ¹⁵N TOCSY-HSQC, HCCH-TOCSY, (H)C(CO)NH-TOCSY, and H(C)(CO)NH-TOCSY [see Clore, G. M. & Gronenborn, A. M. Meth. Enzymol. 239:249-363 (1994);Sattler et al., Prog. in Nuclear Magnetic Resonance Spec. 4:93-158 (1999)].

Stereospecific Methyl Groups: Stereospecific assignments of methyl groups of Valine and Leucine residues can be obtained from an analysis of carbon signal multiplet splitting using a fractionally ¹³C-labeled protein sample, which can be readily prepared using M9 minimal medium containing 10% ¹³C-/90% ¹²C-glucose mixture [see Neri, et al., Biochemistry 28:7510-7516 (1989)].

Dihedral Angle Restraints: Backbone dihedral angle (Φ) constraints can be generated
from the ³J_{HNHα} coupling constants measured in a HNHA-J experiment [see Vuister, G. & Bax, A. J. Am. Chem. Soc. 115:7772-7777 (1993)]. Side-chain dihedral angles (χ1) can be obtained from short mixing time ¹⁵N-edited 3D TOCSY-HSQC [see Clore, et al., J, Biomol. NMR 1:13-22 (1991)] and 3D HNHB experiments [see Matson et al., J. Biomol. NMR 3:239-244 (1993)], which can also provide stereospecific assignments of β methylene protons.

Hydrogen Bonds Restraints: Amide protons that are involved in hydrogen bonds can be identified from an analysis of amide exchange rates measured from a series of 2D ¹H/¹⁵N HSQC spectra recorded after adding ²H₂O to the protein sample.

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NOE Distance Restraints: Distance restraints are obtained from analysis of ¹⁵N, and ¹³C-edited 3D NOESY data, which can be collected with different mixing times to minimize spin diffusion problems. The nuclear Overhauser effect (NOE)-derived

restraints are categorized as strong (1.8-3 Å), medium (1.8-4 Å) or weak (1.8-5 Å) based on the observed NOE intensities. A recently developed procedure for the iterative automated NOE analysis by using ARIA [see Nilges et al., Prog. NMR Spectroscopy 32:107-139 (1998)] can be employed which integrates with X-PLOR for structural calculations. To ensure the success of ARIA/X-PLOR-assisted NOE analysis and structure calculations, the ARIA assigned NOE peaks can be manually confirmed.

Intermolecular NOE Distance Restrains: For the structural determination of a protein/peptide complex, intermolecular NOE distance restraints can be obtained from a 13 C-edited (F_1) and 15 N, and 13 C-filtered (F_3) 3D NOESY data set collected for a sample containing isotope-labeled protein and non-labeled peptide.

Structure Calculations and Refinements: Structures of the protein can be generated using a distance geometry/simulated annealing protocol with the X-PLOR program

[see Nilges, et al., FEBS Lett. 229:317-324 (1988); Kuszewski, et al., J. Biolmol. NMR
2:33-56 (1992); Brünger, A. T. X-PLOR Version 3.1: A system for X-Ray crystallography and NMR (Yale University Press, New Haven, CT, 1993)]. The structure calculations can employ inter-proton distance restraints obtained from 15N-and 13C-resolved NOESY spectra. The initial low-resolution structures can be used to facilitate NOE assignments, and help identify hydrogen bonding partners for slowly exchanging amide protons. The experimental restraints of dihedral angles and hydrogen bonds can be included in the distance restraints for structure refinements.

<u>Protein-Structure Based Design of Agonists and Antagonists</u> <u>of the Bromodomain-Acetyl-Lysine Binding Complex</u>

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Once the three-dimensional structure of the Bromodomain and the Bromodomain-acetyl-lysine binding complex are determined, a potential drug or agent (antagonist or agonist) can be examined through the use of computer modeling using a docking program such as GRAM, DOCK, or AUTODOCK [Dunbrack et al., 1997, supra]. This procedure can include computer fitting of potential agents to the bromodomain, for example, to ascertain how well the shape and the chemical structure of the potential ligand will complement or interfere with the interaction between the bromodomain and

the acetyl-lysine [Bugg et al., Scientific American, Dec.:92-98 (1993); West et al., TIPS, 16:67-74 (1995)]. Computer programs can also be employed to estimate the attraction, repulsion, and steric hindrance of the agent to the dimer-dimer binding site, for example. Generally the tighter the fit (e.g., the lower the steric hindrance, and/or the greater the attractive force) the more potent the potential drug will be since these properties are consistent with a tighter binding constant. Furthermore, the more specificity in the design of a potential drug the more likely that the drug will not interfere with related proteins. This will minimize potential side-effects due to unwanted interactions with other proteins.

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Initially a potential drug could be obtained by screening a random peptide library produced by recombinant bacteriophage for example, [Scott and Smith, Science, 249:386-390 (1990); Cwirla et al., Proc. Natl. Acad. Sci., 87:6378-6382 (1990); Devlin et al., Science, 249:404-406 (1990)] or a chemical library. An agent selected in this manner could be then be systematically modified by computer modeling programs until one or more promising potential drugs are identified. Such analysis has been shown to be effective in the development of HIV protease inhibitors [Lam et al., Science 263:380-384 (1994); Wlodawer et al., Ann. Rev. Biochem. 62:543-585 (1993); Appelt, Perspectives in Drug Discovery and Design 1:23-48 (1993); Erickson,

20 Perspectives in Drug Discovery and Design 1:109-128 (1993)].

Such computer modeling allows the selection of a finite number of rational chemical modifications, as opposed to the countless number of essentially random chemical modifications that could be made, any one of which might lead to a useful drug. Each chemical modification requires additional chemical steps, which while being reasonable for the synthesis of a finite number of compounds, quickly becomes overwhelming if all possible modifications needed to be synthesized. Thus, through the use of the three-dimensional structural analysis disclosed herein and computer modeling, a large number of these compounds can be rapidly screened on the computer monitor screen, and a few likely candidates can be determined without the laborious synthesis of untold numbers of compounds.

Once a potential drug (agonist or antagonist) is identified it can be either selected from a library of chemicals as are commercially available from most large chemical companies including Merck, GlaxoWelcome, Bristol Meyers Squib, Monsanto/Searle, Eli Lilly, Novartis and Pharmacia UpJohn, or alternatively the potential drug may be synthesized *de novo*. As mentioned above, the *de novo* synthesis of one or even a relatively small group of specific compounds is reasonable in the art of drug design.

The potential drug can then be tested in any standard binding assay (including in high throughput binding assays) for its ability to bind to the ZA loop of a bromodomain.

Alternatively the potential drug can be tested for its ability to modulate the binding of a bromodomain to acetylated histamine, for example. When a suitable potential drug is identified, a second NMR structural analysis can optionally be performed on the binding complex formed between the bromodomain-acetyl-lysine binding complex, or the bromodomain alone and the potential drug. Computer programs that can be used to aid in solving such three-dimensional structures include QUANTA, CHARMM, INSIGHT, SYBYL, MACROMODE, and ICM, MOLMOL, RASMOL, AND GRASP [Kraulis, J. Appl Crystallogr. 24:946-950 (1991)]. Most if not all of these programs and others as well can be also obtained from the WorldWideWeb through the internet.

Using the approach described herein and equipped with the structural analysis disclosed herein, the three-dimensional structures of other bromodomain-acetyl-lysine binding complexes can more readily be obtained and analyzed. Such analysis will, in turn, allow corresponding drug screening methodology to be performed using the three-dimensional structures of such related complexes.

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For all of the drug screening assays described herein further refinements to the structure of the drug will generally be necessary and can be made by the successive iterations of any and/or all of the steps provided by the particular drug screening assay, including further structural analysis by NMR, for example.

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Phage libraries for Drug Screening.

Phage libraries have been constructed which when infected into host *E. coli* produce random peptide sequences of approximately 10 to 15 amino acids [Parmley and Smith,

Gene 73:305-318 (1988), Scott and Smith, Science 249:386-249 (1990)]. Specifically, the phage library can be mixed in low dilutions with permissive E. coli in low melting point LB agar which is then poured on top of LB agar plates. After incubating the plates at 37°C for a period of time, small clear plaques in a lawn of E. coli will form which represents active phage growth and lysis of the E. coli. A representative of these phages can be absorbed to nylon filters by placing dry filters onto the agar plates. The filters can be marked for orientation, removed, and placed in washing solutions to block any remaining absorbent sites. The filters can then be placed in a solution containing, for example, a radioactive bromodomain. After a specified incubation period, the filters can be thoroughly washed and developed for autoradiography. Plaques containing the phage that bind to the radioactive bromodomain can then be identified. These phages can be further cloned and then retested for their ability to bind to the bromodomain as before. Once the phage has been purified, the binding sequence contained within the phage can be determined by standard DNA sequencing techniques. Once the DNA sequence is known, synthetic peptides can be generated which are encoded by these sequences. These peptides can be tested, for example, for their ability to modulate the affinity of the bromodomain for its binding partner (e.g., a protein comprising an acetyl-lysine or a fragment of that protein).

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The effective peptide(s) can be synthesized in large quantities for use in *in vivo* models and eventually in humans to treat certain tumors. It should be emphasized that synthetic peptide production is relatively non-labor intensive, easily manufactured, quality controlled and thus, large quantities of the desired product can be produced quite cheaply. Similar combinations of mass produced synthetic peptides have been used with great success [Patarroyo, *Vaccine*, 10:175-178 (1990)].

Drug Screening Assays

The drug screening assays of the present invention may use any of a number of means for determining the interaction between an agent or drug and a peptide comprising an acetyl-lysine and/or a bromodomain. Thus, standard high throughput drug screening procedures can be employed using a library of low molecular weight compounds, for

example that can be screened to identify a binding partner for the bromodoamin. Any such chemical library can be used including those discussed above.

In a particular assay, a bromodomain is placed on or coated onto a solid support.

Methods for placing the peptides or proteins on the solid support are well known in the art and include such things as linking biotin to the protein and linking avidin to the solid support. An agent is allowed to equilibrate with the bromodomain to test for binding. Generally, the solid support is washed and agents that are retained are selected as potential drugs. Alternatively, a peptide comprising an acetyl-lysine is placed on or coated onto a solid support. In a particular embodiment of this type, the peptide comprises the amino acid sequence of SEQ ID NO:4.

The agent may be labeled. For example, in one embodiment radiolabeled agents are used to measure the binding of the agent. In another embodiment the agents have fluorescent markers. In yet another embodiment, a Biocore chip (Pharmacia) coated with the bromodomain is used, for example and the change in surface conductivity can be measured.

In addition, since a number of proteins have been identified that contain

20 bromodomains, and the binding partners of many of these proteins are known, the fact that the bromodomain specifically binds to an acetylated lysine as disclosed herein allows the identification and preparation of a number of potential modulators of the bromodomain-acetyl-lysine binding complex based on the amino acid sequences of the binding partners to the proteins. Such potential modulators include: ISYGR-AcK-

25 KRRQRR (SEQ ID NO:4), ARKSTGG-AcK-APRKQL (SEQ ID NO:5) and QSTSRHK-AcK-LMFKTE (SEQ ID NO:6) which bind to the P/CAF bromodomain as shown in the Example, below. Such peptides also can be used, for example, as a starting point for the design of an inhibitor of the bromodomain-acetyl-lysine binding complex.

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Alternatively, a drug can be specifically designed to bind to the ZA loop of a bromodomain for example, such as the P/CAF bromodomain, and be assayed through NMR based methodology [Shuker et al., Science 274:1531-1534 (1996) hereby

incorporated by reference in its entirety.] In a particular embodiment, analogs of the binding partner of the bromodomain can be used in this analysis. One such peptide has the amino acid sequence of SEQ ID NO:4. In another embodiment of this type, the peptide has the amino acid sequence of SEQ ID NO:5. In another such embodiment of this type, the peptide has the amino acid sequence of SEQ ID NO:6.

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The assay begins with contacting a compound with a ¹⁵N-labeled bromodomain. Binding of the compound with the ZA loop of the bromodomain can be determined by monitoring the ¹⁵N- or ¹H-amide chemical shift changes in two dimensional ¹⁵Nheteronuclear single-quantum correlation (15N-HSQC) spectra upon the addition of the compound to the ¹⁵N-labeled bromodomain. Since these spectra can be rapidly obtained, it is feasible to screen a large number of compounds [Shuker et al., Science 274:1531-1534 (1996)]. A compound is identified as a potential ligand if it binds to the ZA loop of the bromodomain. In a further embodiment, the potential ligand can then be used as a model structure, and analogs to the compound can be obtained (e.g., from the vast chemical libraries commercially available, or alternatively through de novo synthesis). The analogs are then screened for their ability to bind the ZA loop of the bromodomain thus to obtain a ligand. An analog of the potential ligand is chosen as a ligand when it binds to the ZA loop of the bromodomain with a higher binding affinity than the potential ligand. In a preferred embodiment of this type the analogs are screened by monitoring the 15N- or 1H-amide chemical shift changes in two dimensional ¹⁵N-heteronuclear single-quantum correlation (¹⁵N-HSQC) spectra upon the addition of the analog to the ¹⁵N-labeled bromodomain as described above.

In another further embodiment, compounds are screened for binding to two nearby sites on the bromodomain. In this case, a compound that binds a first site of the bromodomain does not bind a second nearby site. Binding to the second site can be determined by monitoring changes in a different set of amide chemical shifts in either the original screen or a second screen conducted in the presence of a ligand (or potential ligand) for the first site. From an analysis of the chemical shift changes the approximate location of a potential ligand for the second site is identified. Optimization of the second ligand for binding to the site is then carried out by screening structurally related compounds (e.g., analogs as described above). When

ligands for the first site and the second site are identified, their location and orientation in the ternary complex can be determined experimentally either by NMR spectroscopy or X-ray crystallography. On the basis of this structural information, a linked compound is synthesized in which the ligand for the first site and the ligand for the second site are linked. In a preferred embodiment of this type the two ligands are covalently linked. This linked compound is tested to determine if it has a higher binding affinity for the bromodomain than either of the two individual ligands. A linked compound is selected as a ligand when it has a higher binding affinity for the bromodomain than either of the two ligands. In a preferred embodiment the affinity of the linked compound with the bromodomain is determined monitoring the ¹⁵N- or ¹H-amide chemical shift changes in two dimensional ¹⁵N-heteronuclear single-quantum correlation (¹⁵N-HSQC) spectra upon the addition of the linked compound to the ¹⁵N-labeled bromodomain as described above.

15 A larger linked compound can be constructed in an analogous manner, e.g., linking three ligands which bind to three nearby sites on the bromodomain to form a multilinked compound that has an even higher affinity for the bromodomain than the linked compound.

20 <u>Identification of New Bromodomains</u>

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By disclosing that protein bound acetyl-lysine is a binding partner for bromodomains, the present invention provides a method of identifying novel proteins that contain bromodomains. In short, a protein fragment or analog thereof comprising an acetyllysine can be used as bait to identify a binding partner that comprises a bromodomain. Any one of a number of procedures can be carried out to identify such a binding partner. One such assay comprises passing a cell extract over the bait peptide which is attached to a solid support. After washing the solid support to remove any non-specific binders, the bromodomain containing protein can be eluted from the solid support with an appropriate eluant. In a particular embodiment, the free bait peptide can be used in the elution. Other methodology includes the use of a yeast two-hybrid system, a GST pull down assay, ELISA, immunometric assays, and a modification of the CORT procedure of Schlessinger *et al.*, (US Patent No. 5,858,686, Issued on

January 12, 1999 which is hereby incorporated by reference in its entirety) for use with the bromodomain-acetyl-lysine binding complex.

Labels:

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Suitable labels include enzymes, fluorophores (e.g., fluorescein isothiocyanate (FITC), phycoerythrin (PE), Texas red (TR), rhodamine, free or chelated lanthanide series salts, especially Eu³⁺, to name a few fluorophores), chromophores, radioisotopes, chelating agents, dyes, colloidal gold, latex particles, ligands (e.g., biotin), and chemiluminescent agents. When a control marker is employed, the same or different labels may be used for the test and control marker gene.

In the instance where a radioactive label, such as the isotopes ³H, ¹⁴C, ³²P, ³⁵S, ³⁶Cl, ⁵¹Cr, ⁵⁷Co, ⁵⁸Co, ⁵⁹Fe, ⁹⁰Y, ¹²⁵I, ¹³¹I, and ¹⁸⁶Re are used, known currently available counting procedures may be utilized. In the instance where the label is an enzyme, detection may be accomplished by any of the presently utilized colorimetric, spectrophotometric, fluorospectrophotometric, amperometric or gasometric techniques known in the art.

20 Direct labels are one example of labels which can be used according to the present invention. A direct label has been defined as an entity, which in its natural state, is readily visible, either to the naked eye, or with the aid of an optical filter and/or applied stimulation, e.g. U.V. light to promote fluorescence. Among examples of colored labels, which can be used according to the present invention, include metallic sol particles, for example, gold sol particles such as those described by Leuvering (U.S. 25 Patent 4,313,734); dye sole particles such as described by Gribnau et al. (U.S. Patent 4,373,932 and May et al. (WO 88/08534); dyed latex such as described by May, supra, Snyder (EP-A 0 280 559 and 0 281 327); or dyes encapsulated in liposomes as described by Campbell et al. (U.S. Patent 4,703,017). Other direct labels include a 30 radionucleotide, a fluorescent moiety or a luminescent moiety. In addition to these direct labeling devices, indirect labels comprising enzymes can also be used according to the present invention. Various types of enzyme linked immunoassays are well known in the art, for example, alkaline phosphatase and horseradish peroxidase,

lysozyme, glucose-6-phosphate dehydrogenase, lactate dehydrogenase, urease, these and others have been discussed in detail by Eva Engvall in Enzyme Immunoassay ELISA and EMIT in *Methods in Enzymology*, **70**:419-439 (1980) and in U.S. Patent 4,857,453.

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Suitable enzymes include, but are not limited to, alkaline phosphatase, β -galactosidase, green fluorescent protein and its derivatives, luciferase, and horseradish peroxidase.

Other labels for use in the invention include magnetic beads or magnetic resonance imaging labels.

Antibodies to Portions of the Bromodomain that Interact with Acetyl-Lysine

According to the present invention, the bromodomains, and more particularly the ZA loops of the bromodomains and fragments thereof can be produced by a recombinant source, or through chemical synthesis, or through the modification of these peptides and fragments; and derivatives or analogs thereof, including fusion proteins, may be used as an immunogen to generate antibodies that specifically interfere with the formation of the bromodomain-acetyl-lysine binding complex. Similarly, antibodies can be raised against peptides that comprise one or more acetyl-lysine residues which also interfere with the formation of the bromodomain-acetyl-lysine binding complex. Such antibodies include but are not limited to polyclonal, monoclonal, chimeric, single chain, Fab fragments, and a Fab expression library.

Various procedures known in the art may be used for the production of the polyclonal antibodies. For the production of antibody, various host animals can be immunized by injection with the peptide having the amino acid sequence of SEQ ID NO:3, for example, or a derivative (e.g., or fusion protein) thereof, including but not limited to rabbits, mice, rats, sheep, goats, etc. In one embodiment, the peptide can be conjugated to an immunogenic carrier, e.g., bovine serum albumin (BSA) or keyhole limpet hemocyanin (KLH). Various adjuvants may be used to increase the immunological response, depending on the host species, including but not limited to Freund's (complete and incomplete), mineral gels such as aluminum hydroxide, surface

active substances such as lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, keyhole limpet hemocyanins, dinitrophenol, and potentially useful human adjuvants such as BCG (bacille Calmette-Guerin) and Corynebacterium parvum.

For preparation of monoclonal antibodies directed toward the peptides or protein 5 fragments of the present invention, or analog, or derivative thereof, any technique that provides for the production of antibody molecules by continuous cell lines in culture may be used. These include but are not limited to the hybridoma technique originally developed by Kohler and Milstein [Nature, 256:495-497 (1975)], as well as the trioma 10 technique, the human B-cell hybridoma technique [Kozbor et al., Immunology Today, 4:72 (1983); Cote et al., Proc. Natl. Acad. Sci. U.S.A., 80:2026-2030 (1983)], and the EBV-hybridoma technique to produce human monoclonal antibodies [Cole et al., in Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, Inc., pp. 77-96 (1985)]. In an additional embodiment of the invention, monoclonal antibodies can be produced in germ-free animals utilizing technology described in PCT/US90/02545. In fact, 15 according to the invention, techniques developed for the production of "chimeric antibodies" [Morrison et al., J. Bacteriol., 159:870 (1984); Neuberger et al., Nature, 312:604-608 (1984); Takeda et al., Nature, 314:452-454 (1985)] by splicing the genes from a mouse antibody molecule specific for the peptide having the amino acid 20 sequence of SEQ ID NO:3, for example, together with genes from a human antibody molecule of appropriate biological activity can be used; such antibodies are within the scope of this invention. Such human or humanized chimeric antibodies are preferred for use in therapy of human diseases or disorders (described infra), since the human or humanized antibodies are much less likely than xenogenic antibodies to induce an 25 immune response, in particular an allergic response, themselves.

According to the invention, techniques described for the production of single chain antibodies [U.S. Patent Nos. 5,476,786 and 5,132,405 to Huston; U.S. Patent 4,946,778] can be adapted to produce specific single chain antibodies. An additional embodiment of the invention utilizes the techniques described for the construction of Fab expression libraries [Huse *et al.*, *Science*, 246:1275-1281 (1989)] to allow rapid and easy identification of monoclonal Fab fragments with the desired specificity.

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Antibody fragments which contain the idiotype of the antibody molecule can be generated by known techniques. For example, such fragments include but are not limited to: the $F(ab')_2$ fragment which can be produced by pepsin digestion of the antibody molecule; the Fab' fragments which can be generated by reducing the disulfide bridges of the $F(ab')_2$ fragment, and the Fab fragments which can be generated by treating the antibody molecule with papain and a reducing agent.

In the production of antibodies, screening for the desired antibody can be accomplished by techniques known in the art, e.g., radioimmunoassay, ELISA (enzyme-linked immunosorbant assay), "sandwich" immunoassays, immunoradiometric assays, gel diffusion precipitin reactions, immunodiffusion assays, in situ immunoassays (using colloidal gold, enzyme or radioisotope labels, for example), western blots, precipitation reactions, agglutination assays (e.g., gel agglutination assays, hemagglutination assays), complement fixation assays, immunofluorescence assays, protein A assays, and immunoelectrophoresis assays, etc. In one embodiment, antibody binding is detected by detecting a label on the primary antibody. In another embodiment, the primary antibody is detected by detecting binding of a secondary antibody or reagent to the primary antibody. In a further embodiment, the secondary antibody is labeled. Many means are known in the art for detecting binding in an immunoassay and are within the scope of the present invention. For example, to select antibodies which recognize a specific epitope of a ZA loop of a bromodomain, for example, one may assay generated hybridomas for a product which binds to a bromodomain fragment containing such an epitope and choose those which do not cross-react with bromodomain fragments that do not include that epitope.

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In a specific embodiment, antibodies that interfere with the formation of the bromodomain-acetyl-lysine complex can be generated. Such antibodies can be tested using the assays described and could potentially be used in anti-cancer therapies.

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Administration

According to the invention, the component or components of a therapeutic composition, e.g., an agent of the invention that interferes with the bromodomain-

acetyl-lysine binding complex such as the peptide having the amino acid sequence of SEQ ID NOs:4, 5, or 6 and a pharmaceutically acceptable carrier, may be introduced parenterally, transmucosally, e.g., orally, nasally, or rectally, or transdermally. Preferably, administration is parenteral, e.g., via intravenous injection, and also including, but is not limited to, intra-arteriole, intramuscular, intradermal, subcutaneous, intraperitoneal, intraventricular, and intracranial administration.

In a preferred aspect, the agent of the present invention can cross cellular and nuclear membranes, which would allow for intravenous or oral administration. Strategies are available for such crossing, including but not limited to, increasing the hydrophobic nature of a molecule; introducing the molecule as a conjugate to a carrier, such as a ligand to a specific receptor, targeted to a receptor; and the like.

The present invention also provides for conjugating targeting molecules to such an
agent. "Targeting molecule" as used herein shall mean a molecule which, when
administered *in vivo*, localizes to desired location(s). In various embodiments, the
targeting molecule can be a peptide or protein, antibody, lectin, carbohydrate, or
steroid. In one embodiment, the targeting molecule is a peptide ligand of a receptor on
the target cell. In a specific embodiment, the targeting molecule is an antibody.

Preferably, the targeting molecule is a monoclonal antibody. In one embodiment, to

Preferably, the targeting molecule is a monoclonal antibody. In one embodiment, to facilitate crosslinking the antibody can be reduced to two heavy and light chain heterodimers, or the $F(ab')_2$ fragment can be reduced, and crosslinked to the agent via the reduced sulfhydryl. Antibodies for use as targeting molecule are specific for a cell surface antigen.

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In another embodiment, the therapeutic compound can be delivered in a vesicle, in particular a liposome [see Langer, Science, 249:1527-1533 (1990); Treat et al., in Liposomes in the Therapy of Infectious Disease and Cancer, Lopez-Berestein and Fidler (eds.), Liss: New York, pp. 353-365 (1989); Lopez-Berestein, ibid., pp. 317-327; see generally ibid.].

In yet another embodiment, the therapeutic compound can be delivered in a controlled release system. For example, the agent may be administered using intravenous

infusion, an implantable osmotic pump, a transdermal patch, liposomes, or other modes of administration. In one embodiment, a pump may be used [see Langer, supra; Sefton, CRC Crit. Ref. Biomed. Eng., 14:201 (1987); Buchwald et al., Surgery, 88:507 (1980); Saudek et al., N. Engl. J. Med., 321:574 (1989)]. In another embodiment, polymeric materials can be used [see Medical Applications of Controlled Release, Langer and Wise (eds.), CRC Press: Boca Raton, Florida (1974); Controlled Drug Bioavailability, Drug Product Design and Performance, Smolen and Ball (eds.), Wiley: New York (1984); Ranger and Peppas, J. Macromol. Sci. Rev. Macromol. Chem., 23:61 (1983); see also Levy et al., Science, 228:190 (1985); During et al., Ann. Neurol., 25:351 (1989); Howard et al., J. Neurosurg., 71:105 (1989)]. In yet another embodiment, a controlled release system can be placed in proximity of the therapeutic target, i.e., the bone marrow, thus requiring only a fraction of the systemic dose [see, e.g., Goodson, in Medical Applications of Controlled Release, supra, vol. 2, pp. 115-138 (1984)]. Other controlled release systems are discussed in the review by Langer 15 [Science, 249:1527-1533 (1990)].

Pharmaceutical Compositions. In yet another aspect of the present invention, provided are pharmaceutical compositions of the above. Such pharmaceutical compositions may be for administration for injection, or for oral, pulmonary, nasal or other forms of 20 administration. In general, comprehended by the invention are pharmaceutical compositions comprising effective amounts of a low molecular weight component or components, or derivative products, of the invention together with pharmaceutically acceptable diluents, preservatives, solubilizers, emulsifiers, adjuvants and/or carriers. Such compositions include diluents of various buffer content (e.g., Tris-HCl, acetate, 25 phosphate), pH and ionic strength; additives such as detergents and solubilizing agents (e.g., Tween 80, Polysorbate 80), anti-oxidants (e.g., ascorbic acid, sodium metabisulfite), preservatives (e.g., Thimersol, benzyl alcohol) and bulking substances (e.g., lactose, mannitol); incorporation of the material into particulate preparations of polymeric compounds such as polylactic acid, polyglycolic acid, etc. or into liposomes. 30 Hylauronic acid may also be used. Such compositions may influence the physical state, stability, rate of in vivo release, and rate of in vivo clearance of the present proteins and derivatives. See, e.g., Remington's Pharmaceutical Sciences, 18th Ed. [1990, Mack Publishing Co., Easton, PA 18042] pages 1435-1712 which are herein

incorporated by reference. The compositions may be prepared in liquid form, or may be in dried powder, such as lyophilized form.

Oral Delivery. Contemplated for use herein are oral solid dosage forms, which are described generally in Remington's Pharmaceutical Sciences, 18th Ed.1990 (Mack Publishing Co. Easton PA 18042) at Chapter 89, which is herein incorporated by reference. Solid dosage forms include tablets, capsules, pills, troches or lozenges, cachets or pellets. Also, liposomal or proteinoid encapsulation may be used to formulate the present compositions (as, for example, proteinoid microspheres reported 10 in U.S. Patent No. 4,925,673). Liposomal encapsulation may be used and the liposomes may be derivatized with various polymers (e.g., U.S. Patent No. 5,013,556). A description of possible solid dosage forms for the therapeutic is given by Marshall, K. In: Modern Pharmaceutics Edited by G.S. Banker and C.T. Rhodes Chapter 10, 1979, herein incorporated by reference. In general, the formulation will include an 15 agent of the present invention (or chemically modified forms thereof) and inert ingredients which allow for protection against the stomach environment, and release of the biologically active material in the intestine.

Also specifically contemplated are oral dosage forms of the above derivatized component or components. The component or components may be chemically modified so that oral delivery of the derivative is efficacious. Generally, the chemical modification contemplated is the attachment of at least one moiety to the component molecule itself, where said moiety permits (a) inhibition of proteolysis; and (b) uptake into the blood stream from the stomach or intestine. Also desired is the increase in overall stability of the component or components and increase in circulation time in the body. An example of such a moiety is polyethylene glycol.

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For the component (or derivative) the location of release may be the stomach, the small intestine (the duodenum, the jejunum, or the ileum), or the large intestine. One skilled in the art has available formulations which will not dissolve in the stomach, yet will release the material in the duodenum or elsewhere in the intestine. Preferably, the release will avoid the deleterious effects of the stomach environment, either by

protection of the protein (or derivative) or by release of the biologically active material beyond the stomach environment, such as in the intestine.

The therapeutic can be included in the formulation as fine multi-particulates in the form of granules or pellets of particle size about 1 mm. The formulation of the material for capsule administration could also be as a powder, lightly compressed plugs or even as tablets. The therapeutic could be prepared by compression.

One may dilute or increase the volume of the therapeutic with an inert material. These diluents could include carbohydrates, especially mannitol, a-lactose, anhydrous lactose, cellulose, sucrose, modified dextrans and starch. Certain inorganic salts may be also be used as fillers including calcium triphosphate, magnesium carbonate and sodium chloride. Some commercially available diluents are Fast-Flo, Emdex, STA-Rx 1500, Emcompress and Avicell.

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Disintegrants may be included in the formulation of the therapeutic into a solid dosage form. Materials used as disintegrates include but are not limited to starch, including the commercial disintegrant based on starch, Explotab. Binders also may be used to hold the therapeutic agent together to form a hard tablet and include materials from natural products such as acacia, tragacanth, starch and gelatin.

An anti-frictional agent may be included in the formulation of the therapeutic to prevent sticking during the formulation process. Lubricants may be used as a layer between the therapeutic and the die wall. Glidants that might improve the flow properties of the drug during formulation and to aid rearrangement during compression also might be added. The glidants may include starch, talc, pyrogenic silica and hydrated silicoaluminate.

In addition, to aid dissolution of the therapeutic into the aqueous environment a

30 surfactant might be added as a wetting agent. Additives which potentially enhance
uptake of the protein (or derivative) are for instance the fatty acids oleic acid, linoleic
acid and linolenic acid.

Nasal Delivery. Nasal delivery of an agent of the present invention (or derivative) is also contemplated. Nasal delivery allows the passage of a peptide, for example, to the blood stream directly after administering the therapeutic product to the nose, without the necessity for deposition of the product in the lung. Formulations for nasal delivery include those with dextran or cyclodextran.

Transdermal administration. Various and numerous methods are known in the art for transdermal administration of a drug, e.g., via a transdermal patch. Transdermal patches are described in for example, U.S. Patent No. 5,407,713, issued April 18, 1995 to Rolando et al.; U.S. Patent No. 5,352,456, issued October 4, 1004 to Fallon et al.; U.S. Patent No. 5,332,213 issued August 9, 1994 to D'Angelo et al.; U.S. Patent No. 5,336,168, issued August 9, 1994 to Sibalis; U.S. Patent No. 5,290,561, issued March 1, 1994 to Farhadieh et al.; U.S. Patent No. 5,254,346, issued October 19, 1993 to Tucker et al.; U.S. Patent No. 5,164,189, issued November 17, 1992 to Berger et al.; U.S. Patent No. 5,088,977 and 5,087,240, both issued February 18, 1992 to Sibalis; U.S. Patent No. 5,008,110, issued April 16, 1991 to Benecke et al.; and U.S. Patent No. 4,921,475, issued May 1, 1990 to Sibalis, the disclosure of each of which is incorporated herein by reference in its entirety.

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It can be readily appreciated that a transdermal route of administration may be enhanced by use of a dermal penetration enhancer, e.g., such as enhancers described in U.S. Patent No. 5,164,189 (supra), U.S. Patent No. 5,008,110 (supra), and U.S. Patent No. 4,879,119, issued November 7, 1989 to Aruga et al., the disclosure of each of which is incorporated herein by reference in its entirety.

Pulmonary Delivery. Also contemplated herein is pulmonary delivery of the pharmaceutical compositions of the present invention. A pharmaceutical composition of the present invention is delivered to the lungs of a mammal while inhaling and traverses across the lung epithelial lining to the blood stream. Other reports of this include Adjei et al. [Pharmaceutical Research, 7:565-569 (1990); Adjei et al., International Journal of Pharmaceutics, 63:135-144 (1990) (leuprolide acetate); Braquet et al., Journal of Cardiovascular Pharmacology, 13(suppl. 5):143-146 (1989)

(endothelin-1); Hubbard et al., Annals of Internal Medicine, Vol. III, pp. 206-212 (1989) (α1-antitrypsin); Smith et al., J. Clin. Invest., 84:1145-1146 (1989) (α-1-proteinase); Oswein et al., "Aerosolization of Proteins", Proceedings of Symposium on Respiratory Drug Delivery II, Keystone, Colorado, March, (1990) (recombinant human growth hormone); Debs et al., J. Immunol., 140:3482-3488 (1988) (interferon-γ and tumor necrosis factor alpha); Platz et al., U.S. Patent No. 5,284,656 (granulocyte colony stimulating factor)]. A method and composition for pulmonary delivery of drugs for systemic effect is described in U.S. Patent No. 5,451,569, issued September 19, 1995 to Wong et al.

A subject in whom administration of an agent of the present invention is an effective therapeutic regiment for cancer, for example, is preferably a human, but can be any animal. Thus, as can be readily appreciated by one of ordinary skill in the art, the methods and pharmaceutical compositions of the present invention are particularly suited to administration to any animal, e.g., for veterinary medical use, particularly for a mammal, and including, but by no means limited to, domestic animals, such as feline or canine subjects, farm animals, including bovine, equine, caprine, ovine, and porcine subjects, wild animals (whether in the wild or in a zoological garden), research animals, such as mice, rats, rabbits, goats, sheep, pigs, dogs, cats, avian species, such as chickens, turkeys, and songbirds.

The present invention may be better understood by reference to the following non-limiting Example, which is provided as exemplary of the invention. The following example is presented in order to more fully illustrate the preferred embodiments of the invention. It should in no way be construed, however, as limiting the broad scope of the invention.

EXAMPLE STRUCTURE AND LIGAND OF A HISTONE ACETYLTRANSFERASE BROMODOMAIN

Introduction

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The bromodomain is a protein motif comprising approximately 110 amino acids that is found in practically all nuclear histone acetyltransferases (HATs) [Jeanmougin *et al.*, Trends in Biochemical *Sciences*, 22:151-153 (1997)]. However, despite the seemingly requisite occurrence of this motif in HATs, their role in these enzymes is unknown. Indeed, although this motif has also been identified in other chromatin proteins, heretofore not even one binding partner for a bromodomain had been identified.

Materials and Methods

Sample preparation: The bromodomain of P/CAF (residues 719-832 of SEQ ID NO:2) 15 was subcloned into the pET14b expression vector (Novagen) and expressed in Escherichia coli BL21(DE3) cells. Uniformly ¹⁵N- and ¹⁵N/¹³C-labelled proteins were prepared by growing bacteria in a minimal medium containing ¹⁵NH₄Cl with or without ¹³C₆-glucose. A uniformly ¹⁵N/¹³C-labelled and fractionally deuterated protein sample was prepared by growing the cells in 75% ²H₂O. The bromodomain was 20 purified by affinity chromatography on a nickel-IDA column (Invitrogen) followed by the removal of poly-His tag by thrombin cleavage. The final purification of the protein was achieved by size-exclusion chromatography. The acetyl-lysine-containing peptides were prepared on a MilliGen 9050 peptide synthesizer (Perkin Elmer) using Fmoc/HBTU chemistry. Acetyl-lysine was incorporated using the reagent 25 Fmoc-Ac-Lys with HBTU/DIPEA activation. NMR samples contained approximately 1 mM protein in 100mM phosphate buffer of pH 6.5 and 5mM perdeuterated DTT and $0.5 \text{ mM EDTA in H}_2\text{O}/^2\text{H}_2\text{O} (9/1) \text{ or }^2\text{H}_2\text{O}$.

NMR spectroscopy: All NMR spectra were acquired at 30°C on a Bruker DRX600 or DRX500 spectrometer. The backbone assignments of the ¹H, ¹³C, and ¹⁵N resonances were achieved using deuterium-decoupled triple-resonance experiments of HNCACB and HN(CO)CACB [Yamazaki et al., J. Am. Chem. Soc. 116:11655-11666 (1994)] recorded using the uniformly ¹⁵N/¹³C-labeled and fractionally deuterated protein. The

side-chain atoms were assigned from 3D HCCH-TOCSY [Clore and Gronenborn, Meth. Enzymol. 239:249-363 (1994)] and (H)C(CO)NH-TOCSY [Logan et al., J. Biolmol. NMR 3:225-231 (1993)] data collected on the uniformly ¹⁵N/¹³C-labeled protein. Stereospecific assignments of methyl groups of the Val and Leu residues were obtained using a fractionally ¹³C-labeled sample [Neri et al., Biochemistry 28:7510-7516 (1989)]. The NOE-derived distance restraints were obtained from ¹⁵N- or ¹³C-edited 3D NOESY spectra. ϕ -angle restraints were determined based on the $^3J_{\rm HN,H}\alpha$ coupling constants measured in a 3D HNHA spectrum [Clore and Gronenborn, Meth. Enzymol. 239:249-363 (1994)]. Slowly exchanging amide protons were identified from a series of 2D ¹⁵N-HSQC spectra recorded after the H₂O buffer was changed to a ²H₂O buffer. The intermolecular NOEs used in defining the structure of the bromodomain/Ac-histamine complex were detected in ¹³C-edited (F₁), ¹³C/¹⁵N-filtered (F₃) 3D NOESY spectrum [Clore and Gronenborn, *Meth. Enzymol*. 239:249-363 (1994)]. All NMR spectra were processed with the NMRPipe/NMRDraw 15 programs and analyzed using NMRView [Johnson and Blevins, J. Biomol., NMR 4:603-614 (1994)].

Structure calculations: Structures of the bromodomain were calculated with a distance geometry/simulated annealing protocol using the X-PLOR program [Brunger, A. X-20 PLOR Version 3.1: A system for X-Ray crystallography and NMR, Yale University Press, New Haven, CT, (1993)]. A total of 1324 manually assigned NOE-derived distance restraints were obtained from the ¹⁵N- and ¹³C-edited NOE spectra. Further analysis of the NOE spectra was carried out by the iterative automated assignment procedure using ARIA [Nilges and O'Donoghue, Prog. NMR Spectroscopy 32:107-139 25 (1998)], which integrates with X-PLOR for structure calculations. A total of 1519 unambiguous and 590 ambiguous distance restraints were identified from the NOE data by ARIA, many of which were checked and confirmed manually. The ARIA-assigned distance restraints were in agreement with the structures calculated using only the manually assigned NOE distance restraints, 28 hydrogen-bond distance restraints for 14 hydrogen bonds, and 54ϕ -angle restraints. The final structure 30 calculations employed a total of 3515 NMR experimental restraints obtained from the manual and the ARIA-assisted assignments, 2843 of which were unambiguously assigned NOE-derived distance restraints that comprise of 1077 intra-residue, 621

sequential, 550 medium-range, and 595 long-range NOEs. For the ensemble of the final 30 structures, no distance and torsional angle restraints were violated by more than 0.3Å and 5°, respectively. The total, distance violation, and dihedral violation energies were $178.7 \pm 2.4 \text{ kcal mol}^{-1}$, $41.6 \pm 0.9 \text{ kcal mol}^{-1}$, and $0.50 \pm 0.06 \text{ kcal mol}^{-1}$. respectively. The Lennard-Jones potential which was not used during any refinement stage, was -526.2 ± 16.8 kcal mol⁻¹ for the final structures. Ramachandran plot analysis of the final structures (residues 727-828) with Procheck-NMR [Laskowski et al., J. Biolmol. NMR 8:477-486 (1996)] showed that $71.0 \pm 0.6\%$, $23.8 \pm 0.6\%$, $3.5 \pm 0.2\%$, and $1.7 \pm 0.2\%$ of the non-Gly and non-Pro residues were in the most favorable, additionally allowed, generously allowed, and disallowed regions, respectively. The 10 corresponding values for the residues in the four α -helices (residues 727-743, 770-776, 785-802, and 807-827) were 88.9 \pm 0.4%, 11.0 \pm 0.4%, 0.1 \pm 0.1%, and 0.0 \pm 0.0%. respectively. The structure of the bromodomain/acetyl-histamine complex was determined using the free form structure and additional 25 intermolecular and 5 15 intra-ligand NOE-derived distance restraints.

Site-directed mutagenesis: Mutant proteins were prepared using the QuickChange site-directed mutagenesis kit (Stratagene). The presence of appropriate mutations was confirmed by DNA sequencing.

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Ligand titration: Ligand titration experiments were performed by recording a series of 2D ¹⁵N- and ¹³C-HSQC spectra on the uniformly ¹⁵N-, and ¹⁵N/¹³C-labelled bromodomain (~0.3mM), respectively, in the presence of different amounts of ligand concentration ranging from 0 to approximately 2.0 mM. The protein sample and the stock solutions of the ligands were all prepared in the same aqueous buffer containing 100mM phosphate and 5mM perdeuterated DTT at pH 6.5.

The full length nucleic acid sequence of the human p300/CBP-associated factor (P/CAF) was obtained from GenBank. Accession No: U57317.2 (SEQ ID NO:1):

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1 ggggccgcgt cgacgcggaa aagaggccgt ggggggcctc ccagcgctgg cagacaccgt
61 gaggctggca gccgccggca cgcacaccta gtccgcagtc ccgaggaaca tgtccgcagc
121 cagggcgcgg agcagagtcc cgggcaggag aaccaaggga gggcgtgtgc tgtggcggcg
181 gcggcagcgg cagcggagcc gctagtcccc tccctctgg gggagcagct gccgccgctg
241 ccgccgccgc caccaccatc agcgcgcgg gcccggccag agcgagccgg gcgagcggc
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301 cgctaggggg agggcggggg cggggagggg ggtgggcgaa gggggcggga gggcgtgggg
           361 ggagggtete getetecega etaceagage eegagggaga eeetggegge ggeggeggeg
           421 cetgacacte ggegeeteet geegtgetee ggggeggeat gteegagget ggeggggeeg
           481 ggccgggcgg ctgcggggca ggagccgggg caggggccgg gcccgggggcg ctgccccgc
 5
           541 ageotgegge getteegeee gegeeeeege agggeteeee etgegeeget geegeegggg
           601 gctcgggcgc ctgcggtccg gcgacggcag tggctgcagc gggcacggcc gaaggaccgg
           661 gaggeggtgg eteggeeega ategeegtga agaaagegea aetaegetee geteegeggg
           721 ccaagaaact ggagaaactc ggagtgtact ccgcctgcaa ggccgaggag tcttgtaaat
           781 gtaatggctg gaaaaaccct aacccctcac ccactccccc cagagccgac ctgcagcaaa
10
           841 taattgtcag totaacagaa tootgtogga gttgtagcca tgccctagct gctcatgttt
           901 cccacctgga gaatgtgtca gaggaagaaa tgaacagact cctgggaata gtattggatg
           961 tggaatatct ctttacctgt gtccacaagg aagaagatgc agataccaaa caagtttatt
          1021 tetatetatt taagetettg agaaagteta tittacaaag aggaaaaeet giggitgaag
          1081 gctctttgga aaagaaaccc ccatttgaaa aacctagcat tgaacagggt gtgaataact
15
          1141 ttgtgcagta caaatttagt cacctgccag caaaagaaag gcaaacaata gttgagttgq
          1201 caaaaatgtt cctaaaccgc atcaactatt ggcatctgga ggcaccatct caacgaagac
          1261 tgcgatctcc caatgatgat atttctggat acaaagagaa ctacacaagg tggctgtgtt
          1321 actgcaacgt gccacagttc tgcgacagtc tacctcggta cgaaaccaca caggtgtttg
          1381 ggagaacatt gcttcgctcg gtcttcactg ttatgaggcg acaactcctg gaacaagcaa
20
          1441 gacaggaaaa agataaactg cctcttgaaa aacgaactct aatcctcact catttcccaa
          1501 aatttctgtc catgctagaa gaagaagtat atagtcaaaa ctctcccatc tgggatcagg
          1561 attttctctc agcctcttcc agaaccagcc agctaggcat ccaaacagtt atcaatccac
          1621 ctcctgtggc tgggacaatt tcatacaatt caacctcatc ttcccttgag cagccaaacg
          1681 cagggagcag cagtcctgcc tgcaaagcct cttctggact tgaggcaaac ccaggagaaa
25
          1741 agaggaaaat gactgattct catgttctgg aggaggccaa gaaaccccga gttatggggg
         1801 atattccgat ggaattaatc aacgaggtta tgtctaccat cacggaccct gcagcaatgc
          1861 ttggaccaga gaccaatttt ctgtcagcac actcggccag ggatgaggcg gcaaggttgg
         1921 aagagcgcag gggtgtaatt gaatttcacg tggttggcaa ttccctcaac cagaaaccaa
         1981 acaagaagat cctgatgtgg ctggttggcc tacagaacgt tttctcccac cagctgcccc
30
         2041 gaatgccaaa agaatacatc acacggctcg tctttgaccc gaaacacaaa acccttgctt
         2101 taattaaaga tggccgtgtt attggtggta tctgtttccg tatgttccca tctcaaggat
         2161 tcacagagat tgtcttctgt gctgtaacct caaatgagca agtcaagggc tatggaacac
         2221 acctgatgaa tcatttgaaa gaatatcaca taaagcatga catcctgaac ttcctcacat
         2281 atgcagatga atatgcaatt ggatacttta agaaacaggg tttctccaaa gaaattaaaa
35
         2341 tacctaaaac caaatatgtt ggctatatca aggattatga aggagccact ttaatgggat
         2401 gtgagctaaa tccacggatc ccgtacacag aattttctgt catcattaaa aagcagaagg
         2461 agataattaa aaaactgatt gaaagaaaac aggcacaaat tcgaaaagtt taccctggac
         2521 tttcatgttt taaagatgga gttcgacaga ttcctataga aagcattcct ggaattagag
         2581 agacaggetg gaaacegagt ggaaaagaga aaagtaaaga geecagagae eetgaecage
40
         2641 tttacagcac gctcaagagc atcctccagc aggtgaagag ccatcaaagc gcttggccct
         2701 tcatggaacc tgtgaagaga acagaagctc caggatatta tgaagttata aggttcccca
         2761 tggatctgaa aaccatgagt gaacgcctca agaataggta ctacgtgtct aagaaattat
         2821 tcatggcaga cttacagcga gtctttacca attgcaaaga gtacaacgcc gctgagagtg
         2881 aatactacaa atgtgccaat atcctggaga aattcttctt cagtaaaatt aaggaagctg
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2941 gattaattga caagtgattt tttttccccc tctgcttctt agaaactcac caagcagtgt 3001 gcctaaagca aggt

The full length protein sequence of the human p300/CBP-associated factor (P/CAF)

- 5 was obtained from GenBank. Accession No: U57317.2, (SEQ ID NO:2):
 - 1 MSEAGGAGPG GCGAGAGAG GPGALPPQPA ALPPAPPQGS PCAAAAGGSG ACGPATAVAA
 - 61 AGTAEGPGGG GSARIAVKKA QLRSAPRAKK LEKLGVYSAC KAEESCKCNG WKNPNPSPTP
 - 121 PRADLQQIIV SLTESCRSCS HALAAHVSHL ENVSEEEMNR LLGIVLDVEY LFTCVHKEED
 - 181 ADTKQVYFYL FKLLRKSILQ RGKPVVEGSL EKKPPFEKPS IEQGVNNFVQ YKFSHLPAKE
- 10 241 RQTIVELAKM FLNRINYWHL EAPSQRRLRS PNDDISGYKE NYTRWLCYCN VPQFCDSLPR
 - 301 YETTQVFGRT LLRSVFTVMR RQLLEQARQE KDKLPLEKRT LILTHFPKFL SMLEEEVYSQ
 - 361 NSPIWDQDFL SASSRTSQLG IQTVINPPPV AGTISYNSTS SSLEQPNAGS SSPACKASSG
 - 421 LEANPGEKRK MTDSHVLEEA KKPRVMGDIP MELINEVMST ITDPAAMLGP ETNFLSAHSA
 - 481 RDEAARLEER RGVIEFHVVG NSLNQKPNKK ILMWLVGLQN VFSHQLPRMP KEYITRLVFD
- 15 541 PKHKTLALIK DGRVIGGICF RMFPSQGFTE IVFCAVTSNE QVKGYGTHLM NHLKEYHIKH
 - 601 DILNFLTYAD EYAIGYFKKQ GFSKEIKIPK TKYVGYIKDY EGATLMGCEL NPRIPYTEFS
 - 661 VIIKKQKEII KKLIERKQAQ IRKVYPGLSC FKDGVRQIPI ESIPGIRETG WKPSGKEKSK
 - 721 EPRDPDQLYS TLKSILQQVK SHQSAWPFME PVKRTEAPGY YEVIRFPMDL KTMSERLKNR
 - 781 YYVSKKLFMA DLQRVFTNCK EYNAAESEYY KCANILEKFF FSKIKEAGLI DK

histamine are shown in Tables 5 and 6, respectively.

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Results

The P/CAF bromodomain represents an extensive family of bromodomains (Figure 1). A large number of long-range nuclear Overhauser enhancement (NOE)-derived

25 distance restraints were identified in the NMR data of the P/CAF bromodomain, yielding a well-defined three-dimensional structure (Figures 2A -2D). Table 1 shows the NMR chemical shift assignment of the P/CAF bromodomain. Table 2 shows the Unambiguous NOE-derived distance restraints. Table 3 shows the Ambiguous NOE-derived distance restraints. Table 4 shows the Hydrogen bond restraints. The NMR structure coordinates of the P/CAF bromodomain in the free and complexed to acetyl-

The structure consists of a four-helix bundle (helices α_Z , α_A , α_B , and α_C) with a left-handed twist, and a long intervening loop between helices α_Z and α_A (termed the ZA loop, Figure 2E). The four amphipathic α -helices are packed tightly against one another in an antiparallel manner, with crossing angles for adjacent helices of ~16-20°. The up-and-down four-helix bundle can adapt two topological folds with opposite

handedness (Figures 2F-2G). The right-handed four-helix bundle fold occurs more commonly and is seen in proteins such as hemerythrin and cytochrome b_{562} . The left-handed fold of the bromodomain structure is less common, but also observed in proteins such as cytochrome b₅ and T4 lysozyme [Richardson, J., Adv. Protein Chem., 34:167-339 (1989); Presnell and Cohen, Proc. Natl. Acad. Sci. USA 86:6592-6596 (1989)]. This topological difference arises from the orientation of the loop between the first two helices (Fig. 2F-2G). The right-handed four-helix bundle proteins have a relatively short hairpin-like connection between the first two helices, which makes the "preferred" turn to the right at the top of the first helix [Richardson, J., Adv. Protein Chem., 34:167-339 (1989); Presnell and Cohen, Proc. Natl. Acad. Sci. USA 86:6592-6596 (1989); Weber and Salemme, Nature 287:82-84 (1980)]. In contrast, proteins with the left-handed fold usually have a long loop after the first helix and often contain additional secondary structural elements at the base of the helix bundle [Richardson, J., Adv. Protein Chem., 34:167-339 (1989); Presnell and Cohen, Proc. Natl. Acad. Sci. USA 86:6592-6596 (1989)]. In the bromodomain structure, this long ZA loop has a defined conformation and is packed against the loop between helices α_B and α_C (termed the BC loop) to form a hydrophobic pocket. These tertiary interactions between the two loops appear to favor the left turn of the ZA loop, resulting in the left-handed four-helix bundle fold of the bromodomain. The hydrophobic pocket formed by loops ZA and BC is lined by residues Val752, Ala757, Tyr760, Val763, Tyr802 and Tyr809 20 (Fig. 2H), and appears to be a site for protein-protein interactions (see below). The pocket is located at one end of the four-helix bundle, opposite to the N- and C-termini of the protein. Interestingly, the ZA loop varies in length amongst different bromodomains, but almost always contains residues corresponding to Phe748, Pro751, Pro758, Tyr760, and Pro767 (Figure 1). The conservation of these residues within the 25 ZA loop as well as residues within the α-helical regions implies a similar left-handed four-helix bundle structure for the large family of bromodomains (Fig. 1).

The modular bromodomain structure supports the idea that bromodomain can act as a functional unit for protein-protein interactions. The observation that bromodomains are found in nearly all known nuclear HATs (A-type) that are known to promote transcription-related acetylation of histones on specific lysine residues, but not present in cytoplasmic HATs (B-type), prompted the determination of whether bromodomains

can interact with acetyl-lysine (AcK). The NMR titration of the P/CAF bromodomain were performed with a peptide (SGRGKGG-AcK-GLGK) derived from histone H4, in which Lys8 is acetylated (Lys8 is the major acetylation site in H4 for GCN5, a yeast homologue of P/CAF). Remarkably, the bromodomain could indeed bind the AcK peptide. Moreover, this interaction appeared to be specific, based on the ¹⁵N-HSOC spectra which showed that only a limited number of residues underwent chemical shift changes as a function of peptide concentration (Figure 3A). Conversely, the NMR titration of the bromodomain with a non-acetylated, but otherwise identical H4 peptide, showed no noticeable chemical shift changes, demonstrating that the interaction 10 between the bromodomain and the lysine-acetylated H4 peptide was dependent upon acetylation of lysine. The dissociation constant (K_D) for the AcK peptide was estimated to be $346 \pm 54 \mu M$. This binding is likely reinforced through additional interactions between bromodomain-containing proteins and target proteins. Notably, many chromatin-associated proteins contain two or multiple bromodomains (Figure 1). 15 Indeed, binding with another lysine-acetylated peptide (RKSTGG-AcK-APRKQ) derived from the major acetylation site on histone H3 (residues 9-20) was also observed. Together, these data demonstrate that the P/CAF bromodomain has the ability to bind AcK peptides in an acetylation dependent manner.

Intriguingly, the bromodomain residues that exhibited the most significant ¹H and ¹⁵N 20 chemical shift changes on peptide binding are located near the hydrophobic pocket between the ZA and BC loops (Figure 3B). Because a similar pattern of amide chemical shift changes was observed with the two different AcK-containing peptides, it was surmised that the hydrophobic cavity is the primary binding site for AcK. This 25 hypothesis was further supported by titration with acetyl-histamine, which mimics the chemical structure of the AcK side-chain (Figure 3C). Both ¹⁵N- and ¹³C-HSQC spectra showed that interaction with acetyl-histamine was also acetylation-dependent, involving the same set of residues that showed chemical shift perturbations with similar concentration dependence. It should be noted that the bromodomain did not 30 bind to the amino acids acetyl-lysine or acetyl-histidine alone, possibly due to the presence of the charged amino, carboxyl, or caboxylate group adjacent to the acetyl moiety (Figure 3C). Taken together, these results strongly suggest that the P/CAF

bromodomain can interact with acetyl-lysine-containing proteins in a specific manner, and that this interaction is localized to the bromodomain hydrophobic cavity.

To identify the key residues involved in bromodomain-AcK recognition, the NMR structure of the P/CAF bromodomain in complex with acetyl-histamine was elucidated. As anticipated, the acetylated moiety binds in the bromodomain hydrophobic pocket (Figure 4). The intermolecular interactions are largely hydrophobic in nature, with the methyl group of acetyl-histamine making extensive contacts with the side-chains of Val752, Ala757, and Tyr760, and the methylene groups of acetyl-histamine displaying specific NOEs to Val752, Ala757, Tyr760, Tyr802, and Tyr809. No intermolecular NOEs were observed for the imidazole ring of acetyl-histamine. From the spectral analysis it is clear that the structure of the bromodomain is very similar in both the free and complex forms.

- It is worth noting that the bromodomain-AcK recognition is reminiscent of the interactions between the histone acetyltransferase Hat1 and acetyl-CoA. Although the binding pockets of these two otherwise structurally unrelated proteins are composed of different secondary structural elements, the nature of acetyl-lysine recognition has striking similarities. In particular, Tyr809, Tyr802, Tyr760, and Val752 in the bromodomain appear to be related to Phe220, Phe261, Val254, and Ile217 of Hat1, respectively, in their interactions with the acetyl moiety. This observation may suggest an evolutionary convergent mechanism of acetyl-lysine recognition between bromodomains and histone acetyltransferases.
- To determine the relative contributions of residues within the hydrophobic cavity in bromodomain-AcK binding, site-directed mutagenesis was used to alter residues Tyr809, Tyr802, Tyr760, and Val752 (Table 7).

Table 7. Structural and Functional Analysis of the P/CAF Bromodomain Mutants

5	Bromodomain Proteins	Structural Integrity ^a	H4 AcK-Peptide Binding $K_{\rm D}$ (μ M) ^b
	Wild-Type	++++	346 ± 54
10	Tyr809Ala	++++	No Binding ^c
	Tyr802Ala	+++	> 10,000 ^d
	Tyr760Ala	+++	> 10,000
15	Val752Ala	++	> 10,000

- a. The effects of mutations on the structural integrity of the bromodomain were assessed by using the ¹⁵N-HSQC spectra. The amide ¹H/¹⁵N resonances of the mutant proteins were compared to those of the wild-type bromodomain to determine if the particular mutations lead to global or local structure disruption. Severe line-broadening of the amide resonances would indicate protein conformational exchange due to a decrease of structure stability resulting from point mutations. Structural integrity of the mutant proteins is expressed here relative to that of the wild-type, using the signs of "++++" for as stable as the wild-type, "+++" for mildly destabilized, "++" for moderately destabilized, and "-" for completely unfolded.
- b. The ligand binding affinity (K_D) of the bromodomain proteins was estimated by following chemical shift changes of amide peaks in the ¹⁵N-HSQC spectra as a
 function of the ligand concentration.
 - c. No detectable ligand binding observed in the NMR titration.
- d. Ligand binding affinity was significantly reduced and beyond the limit for reliable measurements by NMR titration.

Substitution of Ala for Tyr809 completely abrogated the bromodomain binding to the lysine-acetylated H4 peptide, while the Tyr802Ala, Tyr760Ala, and Val752Ala mutants had significantly reduced ligand binding affinity. To assess whether these mutations disrupted the overall bromodomain fold, the ¹⁵N-HSOC spectra of the mutants was compared to that of the wild-type protein. For the Tyr809Ala mutant, the amide chemical shifts were only affected for a few residues near the mutation site. However, mutations of the other residues in the hydrophobic binding pocket perturbed the local protein conformation to greater extents, particularly the ZA loop (Table 7). Thus, the NMR structural analysis and the mutagenesis studies show that Tyr809, which is structurally supported by Trp746 and Asn803 (Fiure 4), is essential for the bromodomain interaction with the acetyl group of acetyl-lysine, while residues of Tyr802, Tyr760, and Val752 likely play both structural and functional roles in the recognition. These residues are highly conserved throughout the bromodomain family (Figure 1), suggesting that recognition of acetyl-lysine may be a feature of bromodomains, in general. Therefore, Val752, Ala757, Tyr760, Tyr802, Asn803, and 15 Tyr809 are key amino acid residues for the P/CAF bromodomain binding to acetyllysine.

Table 8: Amino Acid Sequences of Bromodomains Identified in Figure 1

PROTEIN	SEQ ID	GenBank	PROTEIN	SEQ ID	GenBank
BD	NO:	Acc. No.	BD	NO:	Acc. No.
hsp/CAF	7	U57317	dmFSH-2	25	
hsGCN5	8	U57136	scBDF1-2	26	
ttP55	9	U47321	hsBR140	27	JC2069
scGCN5	10	Q03330	hsSMAP	28	X87613
hsP300	11	A54277	ggPB1-1	29	X90849
hsCBP	12	S39162	ggPB1-2	30	
mmCBP	13	S39161	ggPB1-3	31	
ceYNJ1	14	P34545	ggPB1-4	32	
hsCCG1-1	15	P21675	ggPB1-5	33	
msCCG1-1	16	D26114	spBRO-1	34	S54260
hsCCG1-2	17		spBRO-2	35	
msCCG1-2	18		hsSNF2a	36	S45251
hsRing3-1	19	P25440	hsBRG1	37	S39039
hsORFX-1	20	D26362	ggBRM	38	X91638
dmFSH-1	21	P13709	ggBRG1	39	X91637
scBDF1-1	22	P35817	hsTIF1b	40	X97548
hsRing3-2	23		mmTIF1b	41	X99644
hsORFX-2	24		mmTIF1a	42	S78219
	hsp/CAF hsGCN5 ttP55 scGCN5 hsP300 hsCBP mmCBP ceYNJ1 hsCCG1-1 msCCG1-1 hsCCG1-2 msCCG1-2 hsRing3-1 hsORFX-1 dmFSH-1 scBDF1-1 hsRing3-2	BD NO: hsp/CAF 7 hsGCN5 8 ttP55 9 scGCN5 10 hsP300 11 hsCBP 12 mmCBP 13 ceYNJ1 14 hsCCG1-1 15 msCCG1-1 16 hsCCG1-2 17 msCCG1-2 18 hsRing3-1 19 hsORFX-1 20 dmFSH-1 21 scBDF1-1 22 hsRing3-2 23	BD NO: Acc. No. hsp/CAF 7 U57317 hsGCN5 8 U57136 ttP55 9 U47321 scGCN5 10 Q03330 hsP300 11 A54277 hsCBP 12 S39162 mmCBP 13 S39161 ceYNJ1 14 P34545 hsCCG1-1 15 P21675 msCCG1-1 16 D26114 hsCCG1-2 17 The company of the	BD NO: Acc. No. BD hsp/CAF 7 U57317 dmFSH-2 hsGCN5 8 U57136 scBDF1-2 ttP55 9 U47321 hsBR140 scGCN5 10 Q03330 hsSMAP hsP300 11 A54277 ggPB1-1 hsCBP 12 S39162 ggPB1-2 mmCBP 13 S39161 ggPB1-3 ceYNJ1 14 P34545 ggPB1-4 hsCCG1-1 15 P21675 ggPB1-5 msCCG1-1 16 D26114 spBRO-1 hsCCG1-2 17 spBRO-2 msCCG1-2 18 hsSNF2a hsRing3-1 19 P25440 hsBRG1 hsORFX-1 20 D26362 ggBRM dmFSH-1 21 P13709 ggBRG1 scBDF1-1 22 P35817 hsTiF1b	BD NO: Acc. No. BD NO: hsp/CAF 7 U57317 dmFSH-2 25 hsGCN5 8 U57136 scBDF1-2 26 ttP55 9 U47321 hsBR140 27 scGCN5 10 Q03330 hsSMAP 28 hsP300 11 A54277 ggPB1-1 29 hsCBP 12 S39162 ggPB1-2 30 mmCBP 13 S39161 ggPB1-3 31 ceYNJ1 14 P34545 ggPB1-4 32 hsCCG1-1 15 P21675 ggPB1-5 33 msCCG1-1 16 D26114 spBRO-1 34 hsCCG1-2 17 spBRO-2 35 msCCG1-2 18 hsSNF2a 36 hsRing3-1 19 P25440 hsBRG1 37 hsORFX-1 20 D26362 ggBRM 38 dmFSH-1 21 P13709 ggBRG1 <t< td=""></t<>

The present invention is not to be limited in scope by the specific embodiments described herein. Indeed, various modifications of the invention in addition to those described herein will become apparent to those skilled in the art from the foregoing description and the accompanying figures. Such modifications are intended to fall within the scope of the appended claims.

It is further to be understood that all base sizes or amino acid sizes, and all molecular weight or molecular mass values, given for nucleic acids or polypeptides are approximate, and are provided for description.

5 Various publications are cited herein, the disclosures of which are hereby incorporated by reference herein in their entireties.

N 121.192000	HG11 1.748000 HG12 1.052000 CG2 17.168000 HG2# 1.003000 CD1 13.863000 HD1# 0.619000 END_RES_DEF RES_ID 736 RES_TYPE LEU SPIN_SYSTEM_ID 22 HETEROGENEITY 100 N 119.880000 HN 8.841000 CA 58.473000 HA 4.090000 CB 41.950000 HB1 2.090000 HB2 1.703000 CG 27.330000 HG 1.759000 CD1 26.530000 HG 1.759000 CD1 26.530000 HD2# 0.977000 END_RES_DEF RES_ITYPE GLN SPIN_SYSTEM_ID 23 HETEROGENEITY 100 N 117.256000 HN 8.505000
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SPIN_SYSTEM_ID 3 RES_ID 725 CA 66.730000 HETEROGENEITY 100 RES_TYPE PRO	RES_ID 737 RES_TYPE GLN SPIN_SYSTEM_ID 23 HETEROGENEITY 100 N 117.256000 HN 8.505000
RES_ID 718 CA 65.08000 CG2 21.570000 RES_TYPE MET HA 4.329000 HG2# 1.142000 SPIN_SYSTEM_ID 4 CB 32.590000 END_RES_DEP HETEROGENEITY 100 HB1 2.326000 RES_ID 732 RES_ID 719 HG1 2.028000 SPIN_SYSTEM_ID 18 RES_ID 719 HG1 2.028000 SPIN_SYSTEM_ID 18 RES_TYPE SER CD 51.310000 HETEROGENEITY 100 SPIN_SYSTEM_ID 5 HD1 3.866000 N 120.536000 HETEROGENEITY 100 END_RES_DEF HN 8.460000 END_RES_DEF CA 57.920000 RES_ID 726 HA 3.289000	RES_TYPE GLN SPIN_SYSTEM_ID 23 HETEROGENEITY 100 N 117.256000 HN 8.505000
RES_TYPE MET HA 4.329000 HC2# 1.142000 SPIN_SYSTEM_ID 4 CB 32.590000 END_RES_DEF HETEROGENEITY 100 HB1 2.326000 END_RES_DEF HB2 1.973000 RES_ID 732 RES_ID 719 HG1 2.028000 SPIN_SYSTEM_ID 18 RES_TYPE SER CD 51.310000 HETEROGENEITY 100 SPIN_SYSTEM_ID 5 HD1 3.866000 N 120.536000 HETEROGENEITY 100 END_RES_DEF HN 8.460000 END_RES_DEF CA 57.920000 RES_ID 726 HA 3.289000	N 117.256000 HN 8.505000
HETEROGENEITY 100	
CG 27.632000 RES_TYPE	CA 59.020000 HA 4.032000
SPIN_SYSTEM ID 5 HD1 3.866000 N 120.536000 HETEROGENEITY 100 END_RES_DEF HN 8.460000 END_RES_DEF CA 57.920000 RES_ID 726 HA 3.289000	CB 28.182000 HB1 2.327000
END_RES_DEF CA 57.920000 RES_ID 726 HA 3.289000	HB2 2.263000 CG 34.240000
	HG1 2.536000 HG2 2.461000
RES_ID 720 RES_TYPE ASP CB 39.750000 RES_TYPE LYS SPIN_SYSTEM ID 12 HB1 1.532000	END_RES_DEF RES_ID 738
SPIN_SYSTEM_ID 6 HETEROGENEITY 100 HB2 0.294000 HETEROGENEITY 100 N 119.716000 CG 24.880000	RES_TYPE GLN SPIN_SYSTEM_ID 24_
CA 56.296000 HN 8.397000 HG 1.683000 HA 4.361000 CA 55.720000 CD1 25.429000	HETEROGENEITY 100 N 118.896000
CB 33.140000 HA 4.692000 HD1# 0.469000 HB1 1.882000 CB 40.550000 CD2 19.921000 HB2 1.684000 HB1 2.792000 HD2# -0.193000	HN 8.033000 CA 59.574000
CG 25.430000 HB2 2.730000 END_RES_DEF HG1 1.585000 END_RES_DEF	HA 4.196000 CB 29.835000 HB1 2.482000
HG2 1.433000 RES_ID 733 CD 29.834000 RES_ID 727 RES_TYPE LYS	HB2 2.469000 CG 35.342000
HD1 1.703000 RES_TYPE GLN SPIN_SYSTEM_ID 19 CE 41.960000 SPIN_SYSTEM_ID 13 HETEROGENEITY 100 HE1 3.003000 HETEROGENEITY 100 N 118.568000	HG1 2.840000 HG2 2.467000
HE1 3.003000 HETEROGENEITY 100 N 118.568000 END_RES_DEF N 121.356000 HN 8.563000 HN 8.196000 CA 60.125000	NE2 110.369000 HE21 7.022000 HE22 6.916000
RES_ID 721 CA 55.920000 HA 3.679000 RES_TYPE GLU HA 4.163000 CB 32.588000	END_RES_DEP
SPIN_SYSTEM_ID 7 CB 28.730000 HB1 1.729000 HETEROGENEITY 100 HB1 2.148000 HB2 1.360000	RES_ID 739 RES_TYPE VAL
N 122.990000 CG 34.240000 CG 24.880000 HN 8.317000 HG1 2.524000 HG1 1.280000 CA 54.620000 HG2 2.371000 CD 29.835000	SPIN_SYSTEM_ID , 25 HETEROGENEITY 100 N 119.716000
HA 4.540000 END_RES_DEF HD1 1.585000 CB 29.830000 CE 41.960000	HN 8.526000 CA 67.830000
HB1 2.024000 RES_ID 728 HE1 2.918000 HB2 1.893000 RES_TYPE LEU END_RES_DEF	HA 3.844000 CB 32.030000
CG 35.893000 SPIN_SYSTEM_ID 14 HGL 2.271000 HETEROGENEITY 100 RES_ID 734	HB 2.384000 CG1 23.330000
END_RES_DEF N 121.356000 RES_TYPE SER	HG1# 1.183000 CG2 22.120000
TYPE PRO HA 4.045000 N 113.157000 SPIN_SYSTEM_ID 8 CB 41.400000 HN 7.540000	HG2# 1.033000 END_RES_DEF
HETEROGENEITY 100 HB1 1.847000 CA 61.227000 CA 63.430000 HB2 1.555000 HA 4.281000	RES_ID 740 RES_TYPE LYS
HA 4.393000 CG 27.080000 CB 63.879000 CB 32.030000 HG 1.480000 HB1 4.060000	SPIN_SYSTEM_ID 26 HETEROGENEITY 100
HB1 2.224000 CD1 25.970000 END_RES_DEF HB2 1.880000 HD1# 0.794000 CG 27.630000 CD2 23.226000 RES ID 735	N 114.633000 HN 8.572000
CG 27.530000 CD2 23.226000 RES_ID 735 HG1 2.028000 HD2# 0.786000 RES_TYPE ILE CD 50.760000 END_RES_DEF SPIN_SYSTEM_ID 21	CA 59.574000 HA 3.886000 CB 32.380000
HD2 3.656000 HETEROGENEITY 100 HD1 3.800000 RES_ID 729 N 120.700000	HB1 1.873000
ND_RES_DEP RES_TYPE TYR HN 7.951000	HG1 1.022000
SPIN SYSTEM ID 15 CA 65.080000 RES_ID 723 HETEROGENEITY 100 HA 3.786000	HG1 1.022000 HD1 1.520000 END_RES_DEF

SPIN_SYSTEM_ID 27 HETEROGENEITY 100 N 110.369000 HN 7.557000 CA 59.024000 HA 4.448000 CB 63.980000 HB1 4.004000 END_RES_DEF	RES_TYPE PRO SPIN_SYSTEM_ID 33 HETEROGENEITY 100 CA 64.531000 HA 3.756000 CB 29.835000 HB1 0.487000 HB2 -0.783000 CG 26.530000	END_RES_DEP RES_ID 753 RES_TYPE LYS SPIN_SYSTEM_ID 39 HETEROGENEITY 100 N 129.883000 HN 9.045000 CA 56.310000	CB 39.750000 HB1 2.689000 HB2 2.487000 CD1 133.799000 HD1 5.120000 CE1 118.379000 HE1 6.070000 END_RES_DEF
RES_ID 742 RES_TYPE HIS SPIN_SYSTEM_ID 28 HETEROGENEITY 100 N 125.619000 HN 7.536000 CA 58.473000 HA 1.967000	HGI 0.233000 HG2 -0.931000 CD 50.212000 HD2 1.567000 HD1 2.177000 END_RES_DEF RES_ID 748 RES_TYPE PHE	HA 4.370000 CB 32.880000 HB1 1.873000 HG1 1.435000 HD1 1.673000 HE1 2.985000 END_RES_DEF	RES_ID 761 RES_TYPE TYR SPIN_SYSTEM_ID 47 HETEROGENEITY 100 N 113.157000 HN 8.225000 CA 60.676000 HA 4.101000
CB 32.588000 HB1 2.990000 HB2 2.799000 CD2 118.930000 HD2 4.978000 CE1 138.755000 HE1 7.522000 END_RES_DEP	SPIN_SYSTEM_ID 34 HETEROGENEITY 100 N 113.321000 HN 7.585000 CA 55.719900 HA 4.930000 CB 39.202000 HB1 3.491000	RES_TYPE ARG SPIN SYSTEM_ID 40 HETEROGENEITY 100 N 120.208000 HN 8.054000 END_RES_DEF .	CB 37.550000 HB1 3.189000 HB2 2.801000 CD1 134.901000 HD1 7.342000 CE1 118.930000 HE1 6.646000 END_RES_DEF
RES_ID 743 RES_TYPE GLN SPIN_SYSTEM_ID 29 HETEROGENEITY 100 N 128.571000 HN 8.543000 CA 59.125000 HA 4.209000 CB 29.834000	HB2 2.532000 CD1 133.248000 HD1 7.099000 HE1 7.174000 HZ 7.296000 END_RES_DEF RES_ID 749 RES_TYPE MET SPIN_SYSTEM_ID 35	RES_TYPE THR SPIN_SYSTEM_ID 41 HETEROGENEITY 100 CA 63.430000 HA 4.038000 CB 68.380000 HE 4.293000 CG2 22.670000 HG2# 1.267000 END RES_DEP	RES_ID 762 RES_TYPE GLU SPIN_SYSTEM_ID 48 HETEROGENEITY 100 N 117.912000 HN 7.702000 CA 57.922000 HA 4.209000 CB 29.480000
HB1 2.111000 CG 33.690000 HG1 2.390000 NE2 112.173000 HE21 7.581000 HE22 6.870000 END_RES_DEF	HETEROGENEITY 100 N 117.748000 HN 7.115000 CA 56.820000 HA 4.286000 CB 32.590000 HB1 2.233000 HB2 2.174000	RES_ID 756 RES_TYPE GLU SPIN_SYSTEM_ID 42 HETEROGENEITY 100 N 110.732000 HN 7.209000 CA 56.270000	HB1 2.086000 CG 37.545000 HG1 2.325000 HG2 2.265000 END_RES_DEF RES_ID 763 RES_TYPE VAL SPIN_SYSTEM_ID 49
RES_ID 744 RES_TYPE SER SPIN_SYSTEM_ID 30 HETEROGENEITY 100 N 119.060000 HN 11.668000 CA 60.125000 HA 4.838000 CB 63.980000 HB1 4.334000	CG 33.140000 HG1 2.851000 CE 17.168000 HE# 2.175000 END_RES_DEF RES_ID 750 RES_TYPE GLU SPIN_SYSTEM_ID 36 HETEROGENEITY 100	HA 4.448000 CB 30.930000 HB1 2.174000 HB2 2.000000 CG 36.440000 HG1 2.292000 END_RES_DEF RES_ID 757	HETEROGENEITY 100 N 115.453000 HN 7.135000 CA 63.430000 HA 4.077000 CB 33.690000 HB 2.015000 CG1 21.020000 HG1# 1.045000
HB2 3.926000 END_RES_DEF RES_ID 745 RES_TYPE ALA SPIN_SYSTEM_ID 31 HETEROGENEITY 100 N 117.584000	N 113.813000 HN 7.709000 CA 53.516000 HA 4.849000 CB 31.487000 HB1 2.091000 HB2 1.730000 CG 35.893000	RES_TYPE ALA SPIN_SYSTEM_ID 43 HETEROGENEITY 100 N 122.504000 HN 7.379000 CA 50.220000 HA 4.937000 CB 19.370000 HB# 1.082000	CG2 21.574000
HN 7.868000 CA 53.510000 HA 4.396000 CB 20.470000 HB# 1.688000 END_RES_DEF	HG1 2.164000 END_RES_DEF RES_ID 751 RES_TYPE PRO SPIN_SYSTEM_ID 37 HETEROGENEITY 100 CA 62.879000	END_RES_DEF RES_ID 758 RES_TYPE PRO SPIN_SYSTEM_ID 44 HETEROGENEITY 100 CA 65.080000 HA 4.496000	HN 7.947000 CA 57.92000 HA 3.916000 CB 34.240000 HB 1.205000 CG1 24.878000 HG11 0.798000 HG12 0.216000
RES_TYPE TRP SPIN_SYSTEM_ID 32 HETEROGENEITY 100 N 116.600000 HN 7.135000 CA 60.691000 HA 4.368000 CB 27.630000	HA 4.242000 CB 32.040000 HB1 2.328000 HB2 1.683000 CG 27.080000 HG1 2.126000 HG2 1.978000 CD 50.763000	CB 31.487000 HB1 2.374000 HB2 2.027000 CG 27.632000 HG1 2.122000 HG2 2.038000 CD 50.212000 HD2 3.515000	CG2 16.617000 HG2# 0.380000 CD1 9.457000 HD1# 0.537000 END_RES_DEF RES_ID 765
HB1 3.594000 HB2 3.351000 CD1 128.843000 HD1 7.897000 NE1 110.861000 HEI 10.474000 CE3 122.234000 HE3 7.336000 C22 116.177000	HD1 3.670000 END_RES_DEF RES_ID 752 RES_TYPE VAL SPIN_SYSTEM_ID 38 HETEROGENEITY 100 N 124.450000 HN 8.124000	HD1 3.717000 HD1 3.717000 END_RES_DEF RES_ID 759 RES_TYPE GLY SPIN_SYSTEM_ID 45 HSTEROGENEITY 100 END_RES_DEF	RES_TYPE ARG SPIN_SYSTEM_ID 51 HETEROGEMEITY 100 N 125.291000 HN 7.749000 CA 57.371000 HA 3.875000 CB 30.936000 HB1 1.388000 HB2 1.211000
HZ2 7.382000 CZ3 123.336000 HZ3 7.197000 CH2 126.089000 HH2 7.150000 END_RES_DEF	CA 63.430000 HA 3.553000 CB 32.580000 HB 1.145000 CG1 21.573000 HG1# 0.464000 CG2 21.573000 HG2# 0.169000	RES_ID 760 RES_TYPE TYR SPIN_SYSTEM_ID 46 HETEROGENEITY 100 N 122.504000 HN 7.945000 CA 62.328000 HA 3.536000	HBZ 1.211000 CG 27.080000 HG1 1.319000 HG2 1.173000 CD 41.052000 HD1 2.971000 END_RES_DEF

RES_TYPE SPIN_SYSTEM_ID							
	SER	end_res_dep		CD1 25.42900	00	SPIN_SYSTEM_ID	69
	52			HD1# 1.06700	30	HETEROGENE I TY	100
heterogene i ty	100	RES ID	772	CD2 27.08100		N 115.780000	
N 116.600000		RES TYPE	THR	HD2# 0.87100		HN 7.698000	
HN 8.387000		SPIN SYSTEM ID	58		, ,		
CA 54.618000		HETEROGENEITY		end_res_def		CA 62.330000	
			100			HA 4.083000	
HA 4.984000		N 122.176000	?	RES_ID	778	CB 31.500000	
CB 38.640000		HN 9.445000		RES_TYPE	LYS	HB 2.321000	
HB1 3.034000		CA 67.040000	1	SPIN_SYSTEM_ID	64	CG1 21.57000	0
HB2 2.907000		HA 3.845000		HETEROGENEITY	100	HG1# 0.94400	
END_RES_DEP		CB 67.835000	,	N 120.372000		CG2 18.82000	
		HB 4.090000			•		
RES_ID	767			HN 7.958000		HG2# 0.82300	U
		CG2 22.12400		CA 59.574000		END_RES_DEF	
RES_TYPE	PRO	HG2# 1.05800	0	HA 4.333000			
SPIN_SYSTEM_ID	53	end_res_def		CB 32.588000	1	RES_ID	784
HETEROGENE I TY	100			HB1 2.055000	L	RES_TYPE	SER
CA 63.429000		RES_ID	773	CG 24.878000		SPIN SYSTEM ID	70
HA 4.083000		RES TYPE	MET	HG1 1.596000			
CB 32.588000						HETEROGENE ITY	100
		SPIN_SYSTEM_ID	59	CD 29.835000		N 111.353000	
HB1 2.209000		HETEROGENEITY	100	HD1 1.804000		HN 7.415000	
CG 28.180000		N 117.912000		CE 41.951000		CA 55.719000	
HG1 2.177000		HN 7.882000		HE1 2.990000		HA 4.741000	
HG2 1.883000		CA 60.676000		END_RES_DEF		CB 66.183000	
°CD 50.763000		HA 4.319000				HB1 4.200000	
HD2 3.390000		CB 33.342000		RES ID	779		
						HB2 3.750000	
HD1 3.623000		HB1 2.093000		RES_TYPE	ASN	END_RES_DEP	
END_RES_DEF		HB2 1.915000		SPIN_SYSTEM_ID	65		
		CG 33.139000		HETEROGENE ITY	100	RES_ID	785
	768	HG1 2.621000		N 116.108000			LYS
	MET	HG2 2.496000		HN 7.947000		SPIN SYSTEM ID	
	54	CE 16.620000		CA 53.510000			
						HETEROGENEITY	100
	100	HE# 1.241000		HA 4.771000		CA 59.030000	
N 119.060000		END_RES_DEF		CB 38.095000		HA 4.021000	
HN 8.430000				HB1 3.019000		CB 31.590000	
CA 54.067000		RES ID	774	HB2 2.773000		END_RES_DEF	
HA 4.935000		RES TYPE	SER	ND2 112.6650	00		
CB 31.487000		SPIN SYSTEM ID					
			60	HD21 7.59800			786
HB1 1.989000		haterogene ITY	100	HD22 6.96900	0	RES_TYPE	LYS
НВ2 1.353000		N 116.108000		END_RES_DEF		SPIN_SYSTEM_ID	72
CG 30.930000		HN 7.958000				HETEROGENEITY	100
HG1 2.690000		CA 62.879000		RES ID	780	N 120.208000	
CE 14.414000		HA 4.200000		RES_TYPE	ARG	HN 8.244000	
HE# 1.929000		CB 62.879000		SPIN_SYSTEM_ID	66	CA 59.720000	
end_res_def		HB1 4.368000		HETEROGENEITY	100	HA 4.062000	
		HB2 4.040000		N 114.141000		CB 30.385000	
	769	END_RES_DEF		HN 8.158000		HB1 1.779000	
RES_TYPE	ASP			CA 56.821000		CG 24.530000	م
SPIN SYSTEM ID	55	RES ID	775	HA 4.405000		CD 28.182000	
	100	RES_TYPE	GLU	CB 25.429000		HD1 1.680000	
N 119.060000							
		SPIN_SYSTEM_ID	61	HB1 2.097000		CE 41.670000	
HN 7.365000		HETEROGENEITY	100	HB2 2.022000		HE1 3.137000	
CA 53.516000		N 124.471000		CG 27.632000		HE2 3.045000	
HA 4.745000		HN 8.150000		HG1 1.539000		END_RES_DEF	
CB 44.154000	•	CA 59.570000					
HB1 2.371000				HG2 1.534000			
		WA 4 045000		HG2 1.534000			707
		HA 4.045000		CD 43.050000		RES_ID	787
END_RES_DEF		CB 29.280000		CD 43.050000 HD1 3.060000		RES_ID RES_TYPE	LEU
END_RES_DEF		CB 29.280000 HB1 2.246000		CD 43.050000		RES_ID RES_TYPE	
END_RES_DEF	770	CB 29.280000		CD 43.050000 HD1 3.060000		RES_ID RES_TYPE SPIN_SYSTEM_ID	LEU
END_RES_DEF RES_ID	770 LEU	CB 29.280000 HB1 2.246000 HB2 2.063000		CD 43.050000 HD1 3.060000 HD2 3.024000		RES_ID RES_TYPE SPIN_SYSTEM_ID	LEU 73
END_RES_DEF RES_ID RES_TYPE I	EU	CB 29.280000 HB1 2.246000 HB2 2.063000 CG 36.443000		CD 43.050000 HD1 3.060000 HD2 3.024000 END_RES_DEF	781	RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 118.732000	LEU 73
END_RES_DEF RES_ID RES_TYPE SPIN_SYSTEM_ID S	EU 66	CB 29.280000 HB1 2.246000 HB2 2.063000 CG 36.443000 HG1 2.345000		CD 43.050000 HD1 3.060000 HD2 3.024000 END_RES_DEF RES_ID	781 TYR	RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 118.732000 HN 7.422000	LEU 73
END_RES_DEF RES_ID	EU	CB 29.280000 HB1 2.246000 HB2 2.063000 CG 36.443000 HG1 2.345000 HG2 2.176000		CD 43.050000 HD1 3.060000 HD2 3.024000 END_RES_DEF RES_ID RES_TYPE	TYR	RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 118.732000 HN 7.422000 CA 57.922000	LEU 73
RES_ID RES_TYPE SPIN_SYSTEM_ID SHETEROGENEITY N 116.272000	EU 66	CB 29.280000 HB1 2.246000 HB2 2.063000 CG 36.443000 HG1 2.345000		CD 43.050000 HD1 3.060000 HD2 3.024000 END_RES_DEF RES_ID RES_TYPE SPIN_SYSTEM_ID	TYR 67	RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 118.732000 HN 7.422000 CA 57.922000 HA 4.213000	LEU 73
END_RES_DEF RES_ID	EU 66	CB 29.280000 HB1 2.246000 CG 36.443000 HG1 2.345000 HG2 2.176000 END_RES_DEF		CD 43.050000 HD1 3.060000 HD2 3.024000 END_RES_DEF RES_IDP RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY	TYR	RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 118.732000 HN 7.422000 CA 57.922000 HA 4.213000 CB 43.603000	LEU 73
RES_ID RES_TYPE SPIN_SYSTEM_ID N 116.272000 HN 9.055000 CA 57.922000	EU 66	CB 29.280000 HB1 2.246000 HB2 2.063000 CG 36.443000 HG1 2.345000 HG2 2.176000 END_RES_DEP	776	CD 43.050000 HD1 3.060000 HD2 3.024000 END_RES_DEF RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 116.764000	TYR 67	RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 118.732000 HN 7.422000 CA 57.922000 HA 4.213000	LEU 73
END_RES_DEF RES_ID	EU 66	CB 29.280000 HB1 2.246000 CG 36.443000 HG1 2.345000 HG2 2.176000 END_RES_DEP RES_ID RES_TYPE	776 ARG	CD 43.050000 HD1 3.060000 HD2 3.024000 END_RES_DEF RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 116.764000 HN 8.222000	TYR 67	RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 118.732000 HN 7.422000 CA 57.922000 HA 4.213000 CB 43.603000	LEU 73
END_RES_DEF RES_ID	EU 66	CB 29.280000 HB1 2.246000 CG 36.443000 HG1 2.345000 HG2 2.176000 END_RES_DEP RES_ID RES_TYPE		CD 43.050000 HD1 3.060000 HD2 3.024000 END_RES_DEF RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 116.764000	TYR 67	RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 118.732000 CA 57.922000 CA 57.922000 CA 42.13000 CB 41.603000 HB1 1.996000 HB2 1.891000	LEU 73
END_RES_DEF RES_ID	EU 66	CB 29.280000 HB1 2.246000 CG 36.443000 HG1 2.345000 HG2 2.176000 END_RES_DEF RES_ID RES_TYPE SPIM_SYSTEM_ID	ARG	CD 43.050000 HD1 3.060000 HD2 3.024000 END_RES_DEF RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 116.764000 HN 8.222000	TYR 67	RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 118.732000 CA 57.922000 CA 57.922000 CB 43.603000 HB1 1.996000 HB2 1.891000 CC 27.632000 CC 27.632000	LEU 73
END_RES_DEF RES_ID	EU 66	CB 29.280000 HB1 2.246000 CB 2.063000 CG 36.441300 HG2 2.176000 EMD_RES_DEP RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY	ARG 62	CD 43.050000 HD1 3.050000 HD2 3.024000 END_RES_DEF RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 116.764000 HN 8.222000 CA 60.125000 HA 4.064000	TYR 67	RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 118.732000 CA 57.922000 HA 4.213000 CB 43.603000 HB1 1.996000 HB2 1.891000 CG 27.632000 HG 1.794000	LEU 73
END_RES_DEF RES_ID	EU 66	CB 29.280000 HB1 2.246000 CG 36.443000 HG2 2.345000 EMC2 2.176000 END_RES_DEP RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY EN 120.372000	ARG 62	CD 43.050000 HD1 3.060000 HD2 3.024000 END_RES_DEF RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 116.764000 CM 60.125000 HA 4.064000 CB 40.850000 CB 40.850000	TYR 67	RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 118.732000 CA 57.922000 CA 57.922000 CB 41.603000 CB 41.603000 HB1 1.996000 HB2 1.891000 CG 27.632000 CG 1.794000 CG 1.794000 CD 1.5979000	LEU 73
END_RES_DEF RES_ID	EU 66	CB 29.280000 HB1 2.246000 CG 36.443000 HG2 2.345000 EMC 2.176000 EMD_RES_DEF RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 120.372000 HM 8.391000	ARG 62	CD 43.050000 HD1 3.050000 HD2 3.024000 END_RES_DEF RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 116.764000 HN 8.222000 CA 60.125000 CA 40.404000 CB 40.850000 HB1 2.948000	TYR 67	RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 118.732000 CN 7.422000 CA 57.922000 CA 42.13000 CB 43.603000 HB1 1.996000 CG 27.632000 CG 27.632000 CG 1.794000 CD1 25.979000 HD1# 0.924000	LEU 73
RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 116.272000 HM 9.055000 CB 41.400000 HB1 2.095000 HB2 1.395000 CG 27.080000 HG 1.713000	EU 66	CB 29.280000 HB1 2.246000 CG 36.441000 HG1 2.345000 HG2 2.176000 END_RES_DEP RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY M 120.372000 HN 8.391000 CA 60.676000	ARG 62	CD 43.050000 HD1 3.050000 HD2 3.024000 END_RES_DEF RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 116.764000 HN 8.222000 CA 60.125000 HA 4.064000 CB 40.850000 HB1 2.948000 HB2 2.055000	TYR 67 100	RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 118.732000 CA 57.922000 HA 4.213000 CB 43.603000 HB1 1.996000 HB2 1.891000 CG 27.632000 GG 1.794000 CD1 25.979000 HD1# 0.924000 CD2 23.776000	LEU 73
RES_ID	EU 66	CB 29.280000 HB1 2.246000 CG 36.443000 HG1 2.345000 HG2 2.176000 END_RES_DEP RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY H 120.372000 HN 8.391000 CA 60.676000 HA 3.869000	ARG 62	CD 43.050000 HD1 3.060000 HD2 3.024000 END_RES_DEF RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 116.764000 HN 8.222000 CA 60.125000 HA 4.064000 CB 40.850000 HB1 2.948000 HB2 2.0550000 CD1 134.350000	TYR 67 100	RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 118.732000 CA 57.922000 CA 57.922000 CB 41.603000 CB 41.603000 CB 1.996000 CG 27.632000 CG 27.632000 CG 1.794000 CD1 25.979000 HD2# 0.994000 CD2 23.776000	LEU 73
RES_ID	EU 66	CB 29.280000 HB1 2.246000 CG 36.443000 HG2 2.345000 HG2 2.176000 END_RES_DEP RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY M 120.372000 HN 8.391000 CA 60.676000 HA 3.869000 CB 30.385000	ARG 62	CD 43.050000 HD1 3.050000 HD2 3.024000 END_RES_DEF RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 116.764000 HN 8.222000 CA 60.125000 CB 40.850000 HB1 2.948000 HB1 2.948000 CD1 134.35000 HD1 6.285000 CD1 134.35000	TYR 67 100	RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 118.732000 CA 57.922000 HA 4.213000 CB 43.603000 HB1 1.996000 HB2 1.891000 CG 27.632000 GG 1.794000 CD1 25.979000 HD1# 0.924000 CD2 23.776000	LEU 73
RES_ID	EU 66	CB 29.280000 HB1 2.246000 CG 36.443000 HG1 2.345000 HG2 2.176000 END_RES_DEP RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY H 120.372000 HN 8.391000 CA 60.676000 HA 3.869000	ARG 62	CD 43.050000 HD1 3.060000 HD2 3.024000 END_RES_DEF RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 116.764000 HN 8.222000 CA 60.125000 HA 4.064000 CB 40.850000 HB1 2.948000 HB2 2.0550000 CD1 134.350000	TYR 67 100	RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 118.732000 CA 57.922000 CA 57.922000 CB 41.603000 CB 41.603000 CB 1.996000 CG 27.632000 CG 27.632000 CG 1.794000 CD1 25.979000 HD2# 0.994000 CD2 23.776000	LEU 73
RES_ID	EU 66	CB 29.280000 HB1 2.246000 CG 36.443000 HG2 2.345000 HG2 2.176000 END_RES_DEP RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY M 120.372000 HN 8.391000 CA 60.676000 HA 3.869000 CB 30.385000	ARG 62	CD 43.050000 HD1 3.050000 HD2 3.024000 END_RES_DEF RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 116.764000 HN 8.222000 CA 60.125000 CB 40.850000 HB1 2.948000 HB1 2.948000 CD1 134.35000 HD1 6.285000 CD1 134.35000	TYR 67 100	RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 118.732000 HA 7.422000 CA 57.922000 CB 41.603000 HB1 1.996000 CG 27.632000 HG2 1.891000 CG 27.632000 HG3 1.794000 CD1 25.979000 HD1# 0.924000 CD2 23.776000 HD2# 0.895000 END_RES_DEF	LEU 73
RES_ID	EU 66	CB 29.280000 HB1 2.246000 CG 36.443000 HG1 2.345000 EG2 2.176000 END_RES_DEP RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 120.372000 HN 8.391000 CA 60.676000 HA 3.869000 CB 30.385000 HB1 2.0470000 HB2 1.076000	ARG 62	CD 43.050000 HD1 3.060000 HD2 3.024000 END_RES_DEF RES_ID RES_TYPE SPIN SYSTEM ID HETEROGENEITY N 116.764000 HN 8.222000 CA 60.125000 HA 4.064000 CB 40.850000 HB1 2.948000 HB1 2.948000 HB1 2.955000 CD1 134.35000 HD1 6.2850000 CD1 134.35000 HD1 6.7090000 HE1 6.7090000	TYR 67 100	RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 118.732000 HN 7.422000 CA 57.922000 HA 4.213000 CB 43.603000 HB1 1.996000 CB 21.632000 HG2 1.794000 CD1 25.979000 HD1# 0.924000 CD2 23.776000 HD2# 0.895000 END_RES_DEF	LEU 73 100
RES_ID	EU 66	CB 29.280000 HB1 2.246000 CG 36.441000 HG1 2.345000 HG2 2.176000 END_RES_DEF RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY M 120.372000 HN 8.391000 CA 60.676000 HA 3.869000 CB 30.385000 CB 30.385000 HB1 2.047000 HB2 1.076000 CC 29.284000	ARG 62	CD 43.050000 HD1 3.050000 HD2 3.024000 END_RES_DEF RES_ID RES_TYPE SPIN SYSTEM_ID HETEROGENEITY N 116.764000 HN 8.222000 CA 60.125000 HA 4.064000 CB 40.850000 HB1 2.948000 HB2 2.055000 CD1 134.35000 HD1 6.285000 CEI 118.930000	TYR 67 100	RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 118.732000 CA 57.922000 CA 57.922000 CB 43.603000 HB1 1.996000 CG 27.632000 CG 27.632000 CD1 25.979000 CD1 25.979000 CD2 23.776000 HD2# 0.895000 END_RES_DEF RES_ID RES_TYPE	788 PHE
END_RES_DEF RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 116.272000 HA 4.036000 CB 41.400000 HB1 2.095000 HB2 1.395000 CG 27.080000 HG 1.713000 CD1 27.080000 HD1# 0.940000 CD2 22.675000 HD2# 0.628000 END_RES_DEF	.00 16 7EΩ	CB 29.280000 HB1 2.246000 CG 36.441000 HG1 2.345000 HG2 2.176000 END_RES_DEP RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY M 120.372000 HN 8.391000 CA 60.676000 HA 3.869000 CB 30.385000 CB 30.385000 CB 13.72000 HB1 2.047000 HB1 1.076000 CC 29.284000 HG1 1.722000	ARG 62	CD 43.050000 HD1 3.050000 HD2 3.024000 END_RES_DEF RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 116.764000 HA 8.222000 CA 60.125000 HA 4.064000 CB 40.850000 HB1 2.948000 CD 134.35000 HB1 2.948000 CD1 134.35000 HD1 6.285000 CD1 134.93000 HD1 6.709000 END_RES_DEF	TYR 67 100	RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 118.732000 HN 7.422000 CA 57.922000 CB 41.603000 HB1 1.996000 CG 27.632000 HG2 1.891000 CG 27.632000 HG 1.794000 CD1 25.979000 HD1# 0.924000 CD2 23.776000 ED2# 0.895000 END_RES_DEF RES_ID RES_ID RES_SPIN_SYSTEM_ID	788 PHE 74
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END_RES_DEF RES_ID	JEU 16 10,00 71 YS 7	CB 29.280000 HB1 2.246000 HB2 2.063000 CG 36.443000 HG2 2.176000 END_RES_DEF RES_ID RES_TYPE SPIN_SYSTEM_ID HB120.372000 HA 3.869000 CA 60.676000 HA 3.869000 CB 30.385000 HB2 1.076000 CC 29.284000 HB2 1.076000 CC 29.284000 HB2 2.047000 CD 44.154000 HD2 2.051000 END_RES_DEF RES_ID RES_TYPE SPIN_SYSTEM_ID HBTERGGENEITY	ARG 62 100 777 LEU 63	CD 43.050000 HD1 3.060000 HD2 3.024000 END_RES_DEF RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 116.764000 HN 8.222000 CA 66.125000 HB1 2.948000 HB1 2.948000 HB1 2.948000 HB1 13.4.35000 CD1 134.35000 HD1 6.285000 CD1 134.35000 HD1 6.709000 END_RES_DEF RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 114.633000 HN 8.014000 CA 57.920000 HN 8.014000 CA 57.920000 HN 4.528000 CB 36.443000 CB 36.443000 CB 36.443000 CB 36.443000 CB 36.443000	TYR 67 100 0 0 0 782 TYR 68	RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 118.732000 HN 7.422000 CA 57.922000 HA 4.213000 CB 43.603000 HB1 1.996000 HB2 1.891000 CG 27.632000 HG 1.794000 CD1 25.979000 HD1# 0.924000 CD2 23.776000 HD2# 0.895000 END_RES_DEF RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 118.732000 HN 6.928000 CA 60.676000 HA 3.763000 CB 39.750000 HB1 2.345000 HB2 2.381000 CD1 133.799000	LEU 73 100 888 878 874 100
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END_RES_DEF RES_ID	JEU 16 10,00 71 YS 7	CB 29.280000 HB1 2.246000 HB2 2.063000 CG 36.441000 HG2 2.176000 END_RES_DEF RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 120.372000 HA 3.869000 CA 60.676000 HA 3.869000 CB 30.385000 HB1 2.047000 CC 29.284000 HB2 1.076000 CC 29.284000 HB2 1.2047000 CD 44.154000 HD1 2.578000 HD2 2.051000 END_RES_DEF RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 120.208000 HN 8.856000 CA 58.470000 CC 38.470000 CC 48.856000 CC 58.670000	ARG 62 100 777 LEU 63	CD 43.050000 HD1 3.060000 HD2 3.024000 END_RES_DEF RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 116.764000 HN 8.222000 CA 60.125000 HA 4.064000 CB 40.850000 CB 134.35000 HB1 2.948000 HB1 2.948000 HB1 6.285000 CCD1 118.93000 HB1 6.7099000 END_RES_DEF RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 114.633000 HN 8.014000 CA 57.920000 CA 57.9200000 C	TYR 67 100 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 118.732000 CA 57.922000 CA 57.922000 CB 43.603000 CB 43.603000 CB 1.794000 CC 27.632000 HB1 1.995000 HB2 0.995000 ED1# 0.995000 END_RES_DEF RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 118.732000 HA 3.763000 CA 60.676000 CA 60.676000 CA 39.750000 HB1 2.945000 CB 39.750000 CB 133.799000 CD 133.799000	LEU 73 100 888 878 874 100
RES_ID RES_TYPE IN 116.272000 HA 4.036000 CB 41.400000 HD1# 0.940000 CD2 22.675000 HD2# 0.628000 END_RES_TYPE IN 128.079000 HA 8.738000 CB 32.037000 HA 8.738000 CB 32.037000 HB1 2.30000 CD	JEU 16 10,00 71 YS 7	CB 29.280000 HB1 2.246000 HB2 2.063000 CG 36.4413000 HG1 2.345000 HG2 2.176000 END_RES_DEF RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 120.372000 HN 8.391000 CA 60.676000 HB 1 2.047000 HB1 2.047000 HB2 1.076000 CC 29.284000 HG1 1.722000 HG1 1.722000 HG1 2.578000 HG1 3.856000 CD 44.154000 END_RES_DEF RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 120.208000 HN 8.856000 CA 58.470000 HA 4.651000	ARG 62 100 777 LEU 63	CD 43.050000 HD1 3.050000 HD2 3.024000 END_RES_DEF RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 116.764000 HA 4.064000 CB 40.850000 HB1 2.948000 CB1 134.35000 HB1 6.285000 CB1 118.93000 HB1 6.709000 END_RES_DEF RES_TYPE SPIN_SYSTEM_ID HSTEROGENEITY N 114.633000 HA 4.054000 CB 57.920000 CB 36.443000 HB 3.062000 CB 36.443000 HB 3.062000 CB 133.24800 HB 3.062000 CB 133.24800 CD 120.58200	TYR 67 100 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 118.732000 HN 7.422000 CA 57.922000 CA 57.922000 HA 4.213000 HB1 1.996000 CG 27.632000 HG2 1.891000 CG 17.94000 CD1 25.979000 HD1# 0.924000 CD2 23.776000 HD2# 0.895000 END_RES_DEF RES_ID RES_ID RES_ID N 118.732000 CA 60.676000 HA 3.763000 CB 39.750000 HB1 2.945000 CB 39.750000 HB1 2.945000 HB1 2.945000 HB1 2.945000 HB1 6.928000 CD1 133.799000 HD1 6.928000 CD1 133.799000 HD1 6.928000 CD1 133.799000 HD1 6.928000 CE1 131.596000 HE1 6.928000 END_RES_DEF	T88 PHE 74
RES_ID	JEU 16 10,00 71 YS 7	CB 29.280000 HB1 2.246000 HB2 2.063000 CG 36.441000 HG2 2.176000 END_RES_DEF RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 120.372000 HA 3.869000 CA 60.676000 HA 3.869000 CB 30.385000 HB1 2.047000 CC 29.284000 HB2 1.076000 CC 29.284000 HB2 1.2047000 CD 44.154000 HD1 2.578000 HD2 2.051000 END_RES_DEF RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 120.208000 HN 8.856000 CA 58.470000 CC 38.470000 CC 48.856000 CC 58.670000	ARG 62 100 777 LEU 63	CD 43.050000 HD1 3.060000 HD2 3.024000 END_RES_DEF RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 116.764000 HN 8.222000 CA 60.125000 HA 4.064000 CB 40.850000 CB 134.35000 HB1 2.948000 HB1 2.948000 HB1 6.285000 CCD1 118.93000 HB1 6.7099000 END_RES_DEF RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 114.633000 HN 8.014000 CA 57.920000 CA 57.9200000 C	TYR 67 100 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 118.732000 HA 7.422000 CA 57.922000 CA 57.922000 HB1 1.996000 CB1 2.891000 CC2 27.632000 HB2 1.891000 CD1 25.979000 HD1# 0.924000 CD2 23.7766000 HD2# 0.895000 END_RES_DEF RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 118.732000 HA 3.763000 CB 39.750000 CB 39.750000 HB1 2.945000 HB1 2.945000 HB1 2.945000 HB1 2.945000 HB1 2.945000 HB1 6.928000 CD1 133.799000 HD1 6.400000 CE1 131.596000 HE1 6.928000 END_RES_DEF	LEU 73 100 788 PPHE 74 100
RES_ID RES_TYPE IN 116.272000 HA 4.036000 CB 41.400000 HD1# 0.940000 CD2 22.675000 HD2# 0.628000 END_RES_TYPE IN 128.079000 HA 8.738000 CB 32.037000 HA 8.738000 CB 32.037000 HB1 2.30000 CD	JEU 16 10,00 71 YS 7	CB 29.280000 HB1 2.246000 HB2 2.063000 CG 36.4413000 HG1 2.345000 HG2 2.176000 END_RES_DEF RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 120.372000 HN 8.391000 CA 60.676000 HB 1 2.047000 HB1 2.047000 HB2 1.076000 CC 29.284000 HG1 1.722000 HG1 1.722000 HG1 2.578000 HG1 3.856000 CD 44.154000 END_RES_DEF RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 120.208000 HN 8.856000 CA 58.470000 HA 4.651000	ARG 62 100 777 LEU 63	CD 43.050000 HD1 3.060000 HD2 3.0024000 END_RES_DEF RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 116.764000 HA 4.064000 CB 40.850000 HB1 2.948000 CB1 134.35000 HB1 2.948000 CE1 118.93000 CE1 118.93000 CE1 118.93000 END_RES_DEF RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 114.633000 CA 57.920000 HA 4.28000 CB 36.443000 HB1 3.062000 HB1 3.062000 HB1 3.062000 HB1 2.9070000 CCD 133.24800 HB1 7.175000 CEI 120.582000 HB1 7.2860000	TYR 67 100 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 118.732000 HA 7.422000 CA 57.922000 CA 57.922000 HB1 1.996000 CB1 2.891000 CC2 27.632000 HB2 1.891000 CD1 25.979000 HD1# 0.924000 CD2 23.7766000 HD2# 0.895000 END_RES_DEF RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 118.732000 HA 3.763000 CB 39.750000 CB 39.750000 HB1 2.945000 HB1 2.945000 HB1 2.945000 HB1 2.945000 HB1 2.945000 HB1 6.928000 CD1 133.799000 HD1 6.400000 CE1 131.596000 HE1 6.928000 END_RES_DEF	T88 PHE 74
RES_ID	JEU 16 10,00 71 YS 7	CB 29.280000 HB1 2.246000 HB2 2.063000 CG 36.441000 HG2 2.176000 EMD_RES_DEF RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 120.372000 HA 3.869000 CA 60.676000 HA 3.869000 CB 10.76000 CC 29.284000 HB1 2.047000 HB2 1.076000 CG 29.284000 HG2 0.877000 CD 44.154000 HD1 2.578000 HD2 2.051000 EMD_RES_DEF RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 120.208000 HN 8.856000 CA 58.470000 HA 4.691000 CC 42.6210000 CC 42.62100	ARG 62 100 777 LEU 63	CD 43.050000 HD1 3.050000 HD2 3.024000 END_RES_DEF RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 116.764000 HA 4.064000 CB 40.850000 HB1 2.948000 CB1 134.35000 HB1 6.285000 CB1 118.93000 HB1 6.709000 END_RES_DEF RES_TYPE SPIN_SYSTEM_ID HSTEROGENEITY N 114.633000 HA 4.054000 CB 57.920000 CB 36.443000 HB 3.062000 CB 36.443000 HB 3.062000 CB 133.24800 HB 3.062000 CB 133.24800 CD 120.58200	TYR 67 100 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 118.732000 HN 7.422000 CA 57.922000 HA 4.213000 CB 43.603000 HB1 1.996000 HB2 1.891000 CC 27.632000 HG 1.794000 CD1 25.979000 HD1# 0.924000 CD2 23.776000 HD1# 0.924000 END_RES_DEF RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 118.732000 HN 6.928000 CA 60.676000 HA 3.763000 CB 39.750000 HB1 2.945000 HB1 2.945000 HB1 2.945000 CD1 133.799000 CD1 133.799000 CD1 133.799000 END_RES_DEF RES_ID RES_ID RES_ES_DEF	LEU 73 100 888 89 167
RES_ID RES_DEF RES_ID RES_TYPE ISPIN_SYSTEM_ID SHOPE N 116.272000 HM 9.055000 CA 57.922000 HA 4.036000 CB 41.400000 HB1 2.095000 HB2 1.395000 CG 27.0800000 HG 1.713000 CD1 27.0800000 HD1# 0.940000 CD2 22.675000 HD2# 0.6280000 END_RES_DEF RES_ID 77 RES_TYPE ISPIN_SYSTEM_ID 5 HETEROGENEITY ISPIN_SYSTEM ISPIN_SYSTEM ISPIN_SYSTEM ISPIN_SYSTEM ISPIN_SYSTEM ISPIN_SYSTEM ISPIN_SYSTEM ISPIN_SYSTEM ISPIN_SYSTEM ISPIN	JEU 16 10,00 71 YS 7	CB 29.280000 HB1 2.246000 HB2 2.063000 CG 36.441300 HG1 2.345000 HG2 2.176000 END_RES_DEF RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 120.372000 HA 3.865000 CB 30.385000 CB 30.385000 CB 30.385000 CB 10.385000 CB 20.284000 HG1 1.722000 HG1 1.722000 HG1 2.578000 HG1 3.855000 CD 44.154000 HG1 2.578000 HG2 3.855000 END_RES_DEF RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 120.208000 HN 8.856000 CA 58.470000 HA 4.651000 CB 42.621000 HB1 2.295000	ARG 62 100 777 LEU 63	CD 43.050000 HD1 3.050000 HD2 3.024000 END_RES_DEF RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 116.764000 HA 4.064000 CB 40.850000 HB1 2.948000 CB1 134.35000 HB1 6.285000 CB1 118.93000 HB1 6.709000 END_RES_DEF RES_TYPE SPIN_SYSTEM_ID HSTEROGENEITY N 114.633000 HA 4.054000 CA 57.920000 CB 36.443000 HB 3.062000 CB 36.443000 HB 3.062000 CB 133.24800 HB 3.062000 CB 17150000 CC 133.24800 HB 1 7.286000 CE 1720.58200 HE 1 7.286000 END_RES_DEF	TYR 67 100 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 118.732000 HN 7.422000 CA 57.922000 CA 57.922000 HB1 1.996000 CB2 1.891000 CG 27.632000 HB2 1.891000 CD1 25.979000 HD1# 0.924000 CD2 23.7760000 HD2# 0.895000 END_RES_DEF RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 118.732000 CA 60.676000 HA 3.763000 CB 39.750000 HB1 2.945000 CB 39.750000 HB1 2.945000 CB 133.799000 HB1 2.945000 CB 133.799000 HB1 6.928000 CD1 133.799000 HB1 6.928000 CE1 131.596000 END_RES_DEF RES_ID RES_ID RES_SPIN_SYSTEM_ID RES_SPIN_SYST	T88 PHE 74 COO
RES_ID	JEU 16 10,00 71 YS 7	CB 29.280000 HB1 2.246000 HB2 2.063000 CG 36.441000 HG1 2.345000 HG2 2.176000 END_RES_DEP RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY M 120.372000 HA 3.869000 CA 60.676000 HB 1 2.047000 HB1 2.047000 HB2 1.076000 CC 29.284000 CC 29.284000 CC 29.284000 CD 44.154000 HD1 2.578000 HD2 2.051000 END_RES_DEF RES_ID RES_IDF RES_ITYPE SPIN_SYSTEM_ID HETEROGENEITY N 120.208000 HA 4.691000 CC 42.621000 HB1 2.295000 HB1 2.295000 HB1 2.295000 HB2 1.925000 HB2 1.925000 HB2 1.925000 HB2 1.925000	ARG 62 100 777 LEU 63	CD 43.050000 HD1 3.050000 HD1 3.050000 HD2 3.024000 END_RES_DEF RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 116.764000 HA 4.064000 CB 40.850000 HB1 2.948000 CB1 134.35000 HB1 2.948000 CE1 118.93000 CE1 118.93000 CE1 118.93000 END_RES_DEF RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 114.633000 CA 57.920000 HA 4.28000 CB 36.443000 HB 3.062000 HB 3.	TYR 67 100 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 118.732000 HN 7.422000 CA 57.922000 CA 57.922000 HB1 1.996000 CB1 2.891000 CC2 27.632000 HB2 1.891000 CD1 25.979000 HD1# 0.924000 CD2 23.7766000 HD2# 0.895000 END_RES_DEF RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 118.732000 HN 6.928000 CA 60.676000 HA 3.763000 CB 39.750000	LEU 73 100 888 89 167
RES_ID RES_DEF RES_ID RES_TYPE ISPIN_SYSTEM_ID SHOPE N 116.272000 HM 9.055000 CA 57.922000 HA 4.036000 CB 41.400000 HB1 2.095000 HB2 1.395000 CG 27.0800000 HG 1.713000 CD1 27.0800000 HD1# 0.940000 CD2 22.675000 HD2# 0.6280000 END_RES_DEF RES_ID 77 RES_TYPE ISPIN_SYSTEM_ID 5 HETEROGENEITY ISPIN_SYSTEM ISPIN_SYSTEM ISPIN_SYSTEM ISPIN_SYSTEM ISPIN_SYSTEM ISPIN_SYSTEM ISPIN_SYSTEM ISPIN_SYSTEM ISPIN_SYSTEM ISPIN	JEU 16 10,00 71 YS 7	CB 29.280000 HB1 2.246000 HB2 2.063000 CG 36.441300 HG1 2.345000 HG2 2.176000 END_RES_DEF RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 120.372000 HA 3.865000 CB 30.385000 CB 30.385000 CB 30.385000 CB 10.385000 CB 20.284000 HG1 1.722000 HG1 1.722000 HG1 2.578000 HG1 3.855000 CD 44.154000 HG1 2.578000 HG2 3.855000 END_RES_DEF RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 120.208000 HN 8.856000 CA 58.470000 HA 4.651000 CB 42.621000 HB1 2.295000	ARG 62 100 777 LEU 63	CD 43.050000 HD1 3.050000 HD2 3.024000 END_RES_DEF RES_ID RES_TYPE SPIN SYSTEM ID HETEROGENEITY N 116.764000 HN 8.222000 CA 60.125000 HB 2.948000 HB1 2.948000 HB1 2.948000 HB1 13.435000 CD1 134.35000 HD1 6.2855000 CD1 134.35000 END_RES_DEF RES_ID RES_TYPE SPIN SYSTEM ID HETEROGENEITY N 114.633000 HN 8.014000 CA 57.920000 HN 8.014000 CA 57.920000 HB1 3.062000 HB1 3.062000 HB1 3.062000 HB1 3.062000 HB1 3.062000 CD1 133.24800 CD1 133.24800 CD1 133.24800 CD1 133.24800 CD1 137.286000 CD1 120.58200 END_RES_DEF	TYR 67 100 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 118.732000 HN 7.422000 CA 57.922000 CA 57.922000 HB1 1.996000 CB2 1.891000 CG 27.632000 HB2 1.891000 CD1 25.979000 HD1# 0.924000 CD2 23.7760000 HD2# 0.895000 END_RES_DEF RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 118.732000 CA 60.676000 HA 3.763000 CB 39.750000 HB1 2.945000 CB 39.750000 HB1 2.945000 CB 133.799000 HB1 2.945000 CB 133.799000 HB1 6.928000 CD1 133.799000 HB1 6.928000 CE1 131.596000 END_RES_DEF RES_ID RES_ID RES_SPIN_SYSTEM_ID RES_SPIN_SYST	T88 PHE 74 COO

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HN 8.48900		HETEROGENEITY		HETEROGENE ITY	100	SPIN SYSTEM_I	D 94
CA 59.0200		N 117.91200		N 117.91200	0	HETEROGENEITY	
HA 3.91100		HN 7.013000		HN 7.945000		N 123.4880	00
CB 32.5900 HB1 2.3180		CA 66.73000		CA 57.99200		HN 9.06100	0
HB2 2.2080		HA 3.039000 CB 30.93000		HA 4.250000		CA 59.5740	
CG 33.1400		HB 1.435000		CB 30.38500 HB1 2.17200		HA 4.232000	
HG1 2.9420		CG1 22.1240		HB2 2.00300		CB 29.83500 HB1 2.16900	
HG2 2.6110	00	HG1# 0.4790		CG 36.99400		CG 36.4430	
CE 17.1680	00	CG2 21.5730		HG1 2.40700		HG1 2.52800	
HE# 2.02700	00	HG2# 0.1420	00	HG2 2.20300		END_RES_DEF	••
end_res_def		END_RES_DEF		END_RES_DEF			
RES_ID	700					RES_ID	809
RES TYPE	790 ALA	RES_ID RES_TYPE	796	RES_ID	802	RES_TYPE	TYR
SPIN SYSTEM II		SPIN_SYSTEM_ID	PHE 82	RES_TYPE SPIN SYSTEM ID	TYR	SPIN_SYSTEM_II	
HETEROGENEITY	100	HETEROGENE ITY	100	HETEROGENEITY	88 100	HETEROGENEITY	100
N 119.71600	00	N 116.92800		N 116.60000		N 116.43600 HN 8.072000	
HN 8.000000		HN 6.357000		HN 7.744000		CA 60.12000	
CA 55.17000		CA 58.47000	0	CA 60.676000)	HA 3.834000	
HA 4.084000		HA 4.161000		HA 4.369000		CB 37.55000	0
CB 18.27000 HB# 1.48500		CB 38.09600		CB 41.400000		HB1 3.01800	0
END_RES_DEF	10	HB1 3.09000 HB2 2.94400		HB1 2.929000		HB2 2.73800	
PWP_KP3_PP1		CD1 132.147		CD1 134.9010 HD1 6.989000		CD1 132.698	
RES ID	791	HD1 6.64100		CE1 119.4810		HD1 6.89100	
RES_TYPE	ASP	CE1 131.596		HE1 6.823000		CE1 120.032 HE1 7.01100	
SPIN_SYSTEM_ID		HE1 6.45600	0	END_RES_DEF		END_RES_DEF	•
HETEROGENE ITY	100	CZ 129.3930	00				•
N 119.71600		HZ 6.406000		RES_ID	803	RES_ID	810
HN 7.376000 CA 57.37100		END_RES_DEF		RES_TYPE	ASN	RES_TYPE	TYR
HA 4.37100		RES ID	797	SPIN_SYSTEM_ID	89	SPIN_SYSTEM_ID	
CB 38.64600		RES TYPE	THR	HETEROGENEITY N 115.944000	100	HETEROGENE ITY	100
HB1 2.73000	-	SPIN SYSTEM ID		HN 8.241000		N 119.88000 HN 7.356000	
END_RES_DEF		HETEROGENEITY	100	CA 51.864000		CA 61.77700	
		N 115.289000		HA 5.024000		HA 3.819000	
RES_ID	792	HN 9.047000		CB 40.849000		CB 40.30000	
RES_TYPE	LEU	CA 66.734000)	HB1 3.069000		HB1 3.39000	0
SPIN_SYSTEM_ID HETEROGENEITY	78 100	HA 3.838000	_	HB2 2.907000		HB2 2.500000	
N 119.55000		CB 68.380000 HB 4.210000)	ND2 118.7320		CD1 136.5530	
HN 7.363000	•	CG2 22.12000		HD21 8.31600 HD22 7.80900		HD1 7.094000	
CA 57.92200	0	HG2# 1.29600		END_RES_DEF	•	CE1 119.4810 HE1 7.00000	
HA 3.398000		END_RES_DEF				END_RES_DEF	•
CB 40.299000				RES_ID	804		
HB1 0.757000		RES_ID	798	RES_TYPE	ALA	RES_ID	832
HB2 0.442000 CG 27.632000		RES_TYPE	ASN	SPIN_SYSTEM_ID	90	RES_TYPE	LYS
HG 0.707000	•	SPIN_SYSTEM_ID HETEROGENEITY	84 100	HETEROGENEITY	100	SPIN_SYSTEM_ID	97
CD1 24.32700	0	N 120.700000		END_RES_DEF		HETEROGENEITY N 118.076000	100
HD1# 0.18400	oo -	HN 8.846000		RES ID	805	HN 8.072000	,
CD2 25.97900	00	CA 55.170000		RESTYPE	PRO	CA 60.676000)
HD2# 0.06100	00	HA 4.315000		SPIN_SYSTEM_ID	91	HA 4.204000	-
END_RES_DEF		CB 38.090000		HETEROGENEITY	100	CB 32.588000)
RES ID	793	HB1 2.985000		CA 63.980000		HB1 2.091000	
RES TYPE	GLN	HB2 2.661000 END_RES_DEF		HA 2.422000 HB1 1.949000		CG 25.979000	
SPIN_SYSTEM ID	79	PWD_KE3_DEF		HG1 1.648000		HG1 1.819000 HG2 1.582000	
HETEROGENE I TY	100	RES ID	799	HG2 1.558000		CD 29.834000	
N 114.141000	•	RESTYPE	CYS	CD 50.762000		HD1 1.813000	
HN 8.069000		SPIN_SYSTEM_ID	85	HD2 3.601000		CE 41.963000	
CA 59.024000 HA 3.804000	1	HETEROGENEITY	100	HD1 3.706000		HE1 2.962000)
CB 28.733000		N 116.928000 HN 6.893000		END_RES_DEF		END_RES_DEF	
HB1 2.157000		CA 62.157000		RES_ID	806		
HB2 2.097000		HA 4.405000		RES TYPE	GLU	RES_ID RES_TYPE	812 CYS
CG 35.342000		CB 26.530000			92	SPIN_SYSTEM_ID	98
HG1 2.460000		HB1 3.304000		HETEROGENEITY	100	HETEROGENE ITY	100
NE2 111.3530		HB2 3.032000		N 112.993000		N 116.764000	
HE21 7.31900		end_res_def		HN 8.246000		HN 8.520000	
HE22 7.22200 END_RES_DEP	v	RES ID	800	CA 56.820000 HA 4.185000		CA 65.087000	
		RES_TYPE	LYS	CB 28.733000		HA 4.202000	
RES_ID	794	SPIN_SYSTEM_ID	86	HB1 2.095000		CB 27.080000 HB1 3.396000	
RESTYPE	ARG	HETEROGENE ITY	100	HB2 1.973000		HB2 3.056000	
SPIN_SYSTEM_ID	80	N 116.764000		CG 36.270000		END_RES DEF	
HETEROGENEITY	100	HN 7.799000		HG1 2.200000			
N 118.568000 HN 7.382000		CA 58.473000		END_RES_DEF		RES_ID	813
CA 58.473000		HA 4.204000 CB 32.588000		BEC 12	807	RES_TYPE	ALA
HA 4.078000		HB1 1.743000			807 SER	SPIN_SYSTEM_ID	99
CB 29.835000		CG 25.429000		-	93	HETEROGENEITY N 120.700000	100
HB1 1.973000		HG1 1.313000			100	HN 8.315000	
HB2 1.886000		HG2 0.138000		N 115.780000		CA 55.563000	
CG 27.080000	•	CD 29.835000		HN 8.112000		HA 3.834000	
HG1 1.742000 CD 43.603000		HD1 1.291000		CA 58.473000		CB 18.270000	
HD1 3.390000		CE 41.400000 HE1 2.486000		HA 4.406000		HB# 1.597000	
HD2 3.325000		HE2 2.421000		CB 66.183000 HB1 4.393000		END_RES_DEF	
END_RES_DEF		END_RES_DEF		HB2 4.157000	•	RES_ID	814
. –				END_RES_DEF		RES TYPE	ASN
RES_ID	795 .		801				100
RES_TYPE	VAL		GLU			HETEROGENEITY	100
SPIN_SYSTEM_ID	81	SPIN_SYSTEM_ID	87	RES_TYPE	GLU	N 115.453000	

HN 8.068000 CA 56.27000 HA 4.329000 CB 38.64600 HB1 2.87700 HB2 2.83400 END_RES_DEF	o o o	RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 120.70000 HN 9.126000 CA 60.691000 HA 3.961000	0	HB1 1.879000 HB2 1.757000 CG 24.878000 HG1 1.390000 CD 29.284000 HD1 1.633000		END_RES_DEF RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 125.450000	832 LYS 118 100
RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 119.88000 HN 7.912000 CA 65.08000 HA 3.646000 CB 39.197000	100	CB 38.64000 HB1 3.28900 HB2 3.067001 CD1 133.248 HD1 6.904001 CE1 132.698 HB1 7.011000 END_RES_DEF	0 0 0 0 0 0 0 0	CE 41.40000 HE1 2.913000 END_RES_DEF RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 121.192000 HN 8.063000	826 GLU 112 100	HN 7.774000 CA 57.720000 HA 4.082000 CB 33.410000 END_RES_DEF	
HB 1.924000 CG1 29.2840 HG11 1.8820 HG12 1.2010 CG2 17.71800 HG2# 1.01700 *CD1 13.86300 HD1# 0.94000 END_RES_DEP	00 00 00 00 00	RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 118.076000 HN 8.359000 CA 61.770000 HA 3.840000 CB 38.090000	,	CA 59.024000 HA 3.995000 CB 29.834000 HB1 2.058000 CG 36.050000 HG1 2.342000 HG2 2.205000 END_RES_DEP			
RES_ID RES_TYPE		HB1 3.064000 CD1 133.2480 HD1 7.175000 CE1 132.6980 HE1 7.294000 CZ 131.59600 HZ 7.430000 END_RES_DEF	00		827 ALA 113 100		٠
CB 41.951000 HB1 1.405000 HB2 1.199000 CG 26.530000 HG 1.580000 CD1 24.32700 HD1# 0.70100 CD2 25.42900 HD2# 0.69600	0 0	RES_ID RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 114.961000 CA 61.773000 CA 62.879000 CB 62.879000	822 SER 108 100	HB# 1.358000 END_RES_DEF RES_ID RES_TYPE SPIN_SYSTEM_ID	828 GLY 114 100		
END_RES_DEF RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 120.700000 HN 8.073000	817 GLU 103 100	HB1 4.007000 END_RES_DEF RES_ID RES_TYPE	823 LYS 109	CA 45.902000 HA1 4.019000 HA2 3.935000 END_RES_DEF RES_ID RES_TYPE	829 LEU		متر
CA 60.125000 RA 3.185000 CB 29.835000 HB1 1.720000 HB2 1.310000 CG 37.545000 HG1 2.001000 HG2 1.922000 END_RES_DEF		HN 7.938000 CA 56.820000 HA 4.008000 CB 31.487000 HB1 1.730000 CG 23.226000 HG1 0.833000 CD 27.080000			115		
SPIN_SYSTEM_ID	818 LYS 104 100	HD1 1.403000 CE 42.501000 HE1 2.569000 HE2 2.422000 END_RES_DEF	824		130 LE 1.6		
CA 59.688000 HA 4.075000 CB 32.588000 HB1 1.929000 CG 25.644000 HG1 1.492000 CD 29.284000 HD1 1.681000 CE 41.963000 HE1 2.964000 END_RES_DEF		RES_TYPE SPIN_SYSTEM_ID	ILE	HETEROGENEITY 1 N 115.453000 CA 60.676000 HA 7.458000 CB 39.748000 HB 1.810000 CG1 27.080000 HG11 1.314000 CG2 17.718000			
RES_TYPE SPIN_SYSTEM_ID HETEROGENEITY N 121.028000	819 PHE 105 100	CG2 18.820000 HG2# 0.654000 CD1 13.312000 HD1# 0.541000 END_RES_DEF		HG2# 0.815000 CD1 13.312000 HD1# 0.794000 END_RES_DEF	31		
HN 7.869000 CA 61.230000 HA 4.328000 CB 39.200000 HB1 3.133000 CD1 133.80000 HD1 7.180000 END_RES_DEF		RES_TYPE I	325 LYS L11 L00	RES_TYPE A SPIN_SYSTEM_ID 1	SP 17 00		

بالمجمد سيدانه ،

Unambiguous NOE-derived Inter-proton Distance Restraints

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7.704	46.	5 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	3.143	4 6	1.689 7.816	. 900	5.053	2.41	2.790	2.208	£.441 9.113	4.411	4.010
8.857 ppm2	6 . 924 ppm2	6.572 ppm2	11.082 ppm2	8.001 ppm2	6.001 ppm2 6.001 ppm2	7.822 ppm2	7.824 ppm2	7.821 pps2	7.821 ppm2	6.936 ppm2	8.936 ppm2	9.125 ppm2	9.125 ppm2
0.16756E+02 ppm.1 0.50220E+02 ppm.1	0.43992E+02 ppm1		0.21846£+02 ppm1	0.52965E+03 ppm1	0.334216+03 ppm1 0.109538+04 ppm1	0.14380K+03 ppm1	0.30790&+03 ppm1	0.47343E+03 ppm1	0.13090E+03 ppm1	0.906a7E+03 ppm1	0.45\$02E+03 ppm1	0.72592E+03 ppm1	0.15487E+03 ppm1
volume	volume	vol uma	0.11000K+01 volume 0.		volume	volume	volume	volum•		volume	volume	0.11000E+01 volume 0.7	0.11000E+01 volume 0.1
HN)) HDV) weight HD22)) KEV)	MED 1) Weight 0.11000E+01 HN) HD) Weight 0.11000E+01 Weight 0.11000E+01	HBI !!	KE1)) KG2)) Weight HE1)) HG1))		HM)) Weight 0.11000E-01	HB)) HB)) weight 0.11000E+01	.3	HB2)) Weight 0.11000E+01 HB3)) Weight 0.11000E+01 HB3)) Weight 0.11000E+01		HB4)) Weight 0.11000E+01 HB4)) HM))		HN)) HA }) Weight 0.11000	HB1)) HB1)) weight 0.11000
and name and name peak 2141 and name and name	sid 89 and name 1.500 peak 13271 sid 46 and name 144 and name 2.000 peak 8521	and name and name pack 14401 and name	and name and name peak 15611 and name and name	and name and name peak 1 and name and name	and name and name peak 21	and name and name peak, 31	and name and name peak 41	and name and name peak 51 and name and name and name	and name and name peak 71	and name and name and name and name	and name and name peak 121	and hame and name peak 133	and name and name peak 141
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		ASSI (14401) (eqs)4d 'BFD' and r (eqs)4d 'BFD' and r), 700 3, 400 OR (14401) (eqs)4d 'BFD' and r (eqs)4d 'BFD' and r (fass)11	((aegid "E ((aegid "E (aegid "E (aegid "E (aegid "E	(segid "BrD (segid "BrD 2,700 2 ASSI (11) (segid "BrD (segid "BrD 2,600 1	ASSI { 21 } (1 e-gid "8 (1 e-gid "8 (1 e-gid "8 2.20)	((eegid *B ((eegid *B) 300				((segid 'B (segid 'B 2.400 ASSI (101) ((segid 'B (segid 'B	AESI (121) ((eegid 'B ((eegid 'B 2.700	((eegid "B ((eegid "B ((eegid "B 2.500	B. P1500))

	3.686	5.451	. 33	4.538	9.150		2.712	919	\$.003	101	69.	3.596		91.6	ţ	4.201	3.95		Š	3.740	6.476	4.86	3.43	
	9.125 ppm3	12.275 ppm2	12.275 ppm2	12.275 ppe2		9.151 pom.2	8.152 ppm2	6.479 ppm2	6.479 ppm2	6,480 post	9. 166 ppm2	6.166 bon2	0.165 pon2	8.166 ppm2	7. 739 ppm2	7.740 ppm2	7.739 ppm2	12.275 ppm2	6.488 ppm2	6.487 ppm2	9.740 ppm2	9.740 ppm2	9.740 ppm2	
	0.952738+03 ppm1	0.20628\$+03 ppm1	0.16806E+03 ppm1	0.40863E-03 ppm1	0.15134E+03 ppm1	0.44648E+03 ppm1	0.39478E+03 ppm1	0.12405K+03 ppm1	0.13933£+03 ppm1	0.88455£+03 ppm1			0.53058K+03 ppm1	0.11688E+03 ppm1	0.66621E+03 ppm1	0.308728+03 ppm1	0.59972E+03 ppm1	0.41861E+03 ppm1	0.22043E+03 ppm1	0.42542E+01 ppm1	0.44967K+03 ppm1	0.553948+03 ppm1	0.71565E.G3 ppm1	
	11000E-01 volume	11000E-01 volume	11000E-01 volume	0.115GGE+61 volume	0.11000£+01 volume	0.11000E+01 volume	0.11000E+01 volume	0.11050E-61 volume	0.11000E+01 volume			0.11000E+01 volume (0.11000E+01 volume	0.11000K+01 volume (0.11000£+01 volume (1000£-01 volume (0.11000E+01 volume (o 11000E-01 volume C	0.110008*01 volume 0	0.11000E+01 volume 0	0.11000E+01 volume 0	0.110005+01 volume 0	0.11000E+01 volume 0	
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	resid 96 and resid 98 and 1.400 peak	reeld 30 and reeld 30 and 2.400 peak	resid 30 and resid 30 and 2.300 peak	resid 30 and resid 30 and 2.000 peak	resid 30 and resid 29 and 2.200 peak	resid 29 and resid 29 and 1.800 peak	resid 29 and resid 29 and 2.000 peak	resid 31 and resid 39 and 2.100 peak	resid 31 and resid 31 and 2.200 peak	resid 31 and resid 31 and 1.400 peak	resid 2s and resid 2s and 1.600 peak	resid 28 and resid 28 and 1.600 peak	resid 28 and resid 28 and 1.800 peak	resid 28 and resid 29. and 2.100 peak	esid 32 and esid 32 and 1.700 peak	esid 32 and esid 32 and 2.100 peak	esid 32 and esid 32 and 1.700 peak	resid 30 and resid 31 and 2.000 peak	resid 105 and resid 105 and 2.400 peak	esid 105 and esid 105 and 2.000 peak	esid 106 and esid 105 and 1.800 peak	seid 106 and seid 106 and 1.700 peak	resid 106 and n resid 106 and n 1.600 peak	resid 106 and n
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7.983

4.612 ppm2

0.11000E+01 volume 0.57821E+03 ppm1

4.980

7.996 ppm2

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volume

7.996 ppm2

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volume

741) 314 BED and res	and reald 39 and and reald 30 and reald 37 and reald 37 and and reald 37 and and reald 37 and	and resid 97 and 200 peak and resid 98 and 200 peak and seek and seek and seek and seek and	100 and read 56 and 1.00 peak 1.00 peak 1.00 and read 56 and 1.00 peak 1.00 peak 1.00 peak 1.00 peak 1.00 and read 56 and 1.00 peak 1	1.700 peak 1.700 peak 1.700 peak 1.700 peak	TO and resid 95 and 2.400 peak TO and resid 95 and TO and resid 95 and TO and resid 95 and 2.000 peak	######################################	150 2.00 and resid ** and name and a	TED and resid 93 2.700 2.200 2.700 2.200 TED and resid 92 TED and resid 92 TED 1.600 1.600	1001 1001 1000	egid (87) and resid 74 and name 1.20 1.30 1.20 ptx 1041 1.01 1.20 2.20 ptx 1041 1.20 2.20 2.20 ptx 1041 2.20 2.20 2.20 2.20 ptx 1041 2.20 2.20 2.20 2.20 2.20 2.20	2 4 4 5 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5
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9.740 ppm2	6.980 pps2	8.960 ppm2 8.529 ppm2	8.526 ppm2	6.572 ppm2		6.572 ppm2	8.168 ppm2 8.168 ppm2	8.714 ppm2	6.668 ppm2	8.668 ppm2	8.219 ppm2 8.376 ppm2 8.219 ppm2
0.11996E+04 ppml	0.11255£403 ppm1	0.16715E+03 ppm1 0.57313E+03 ppm1	0.52916E+03 ppm1 0.97994E+03 ppm1	0.11922E+04 ppml		414428.	0.17690E+03 ppml	0.38641E+03 ppm1	0.121146+03 ppm1 0.96511R+02 ppm1	0.154176+04 ppml	0.42782E+03 ppm1
0.110008.01 volume	0.11000E+01 volume 0.11000E+01 volume	0.11000E+01 volume	0.11500E+01 volume	0.11000£.01 volume 0.11000K.01 volume	0.11000E+01 volume		0.11000E+01 volume 0.11000E+01 volume	0.11000E+01 volume		0.11000E+01 volume 0.11000E+01 volume	0.11000E+01 volume 0.11000E+01 volume 0.11000E+01 volume
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3.422

8.669 ppm2

volume

pp.

0.11000E.01 volume

. 66

6.936 ppm2

volume

4.80 9.124

8.676 ppm2

8.672 ppm2

0.25513E+03 ppm1

1.977 ppm2

0.65098E.03 ppm1

1.995

7.976 ppm2

0.42091E+03 ppm1

vol ume

3.112

7.979 ppm2

6.678

7.979 ppm2

0.67038E+03 ppm1

0.11000E+01 volume

1.1

8.669 ppm2

0.22376E+03 ppm1 0.37061E+03 ppml

volume

3.598

1.669 ppm2

volume

1.11

0.13528E+03 ppm1

0.11000E-01 volume

3.346

1.669 ppm2 9.679 ppm2 670

9.679 ppm2

0.950548+02 ppm1 0.16612E+03 ppml

volume

5.037

6.713 ppez

volume

0.11000E.01

4.753

8.713 ppm2

6.873 ppm2

0.71435E+03 ppm1

0.11000E+01 volume

0.11000£+61 volume

. 671 ppm2

611 ppm2

vol ume

6.612 ppm3

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0.11000E.01 volume

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1	228	(1401) segid 'BrD segid 'BrD	(1411)	2.400 1.411)	9 8	segid BrD -	(1451) #egid "BrD : #egid "BrD :	7.200 (1461) **914 *B	2.500 1.	megid 'BrD - megid 'BrD - 2.600 1.7	1481 }	To	egid 'BrD '	1501	segid BrD 2,300	- i	, .	egid BrD		. dra' brg.	1561 1914 - BrD -	1900 2.10	0.04. P1	2.700 1.80 (1581)	-	segid 'BrD	ä			0.0	2.900 2.100 [1641] Begid BrD an	• -	8.0 2.40	4
-	117			2.400 NBSI (1433 (eegid	5.7	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1			2 7 -		- 8	7.00	-••	5.2	2.30	- F			. ~ ~		4	• ~~	916	2.70	2.700 2.700		091)	2 600	916	P 50	9 1 E	1650	900	166.
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3	9.104 ppm2	9.106	9.106 ppm2	9.106	3	. 10	613	7.536		7.516 ppm2	7. 535 ppm2		7. 536 p	9.105		8.040 p		6.039 PI	306	<u>.</u>	6.306 pg		6.306 pg	8.306 ppm2	į	:	26 ppm2	36 ppm2		S ppm2	17 ppm2	12 ppm2		8.632 ppm2
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2.000	2 2 2	Q Q	2.100	ş 1	1 3	3 4 9	9 0	2 2	38	9 p	3		P. 1	9	P 2	2	P 0	r pu	P 00	i pu	: :	2	pod	8	P P C	25	. 2	20	2 2 a	5 4	. 2	1	2 2 2 2 c	,
6.2	66	2.0	. 66	,	2	22	20		9	29	; ;	9	99	~	66	6		e	ē.	66		2 6 7	2.0	2.3	e e ~	6.6	•	2.600	***			. î	# # Q	:
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3.549 1.129 100.4 3.627 1.362 2.659 8.765 4.527 1.13 4.669 4.367 2.538 4.712 2.486 4.645 3.143 3.93 7.663 6.622 ppm2 4.832 ppm2 6.612 ppm2 1. 133 ppm2 0.626 ppm2 4.564 ppm2 0.565 ppm2 4.763 ppm2 1.566 ppm2 8.564 ppm2 8.565 ppm2 . 546 pp... 4.146 ppm2 6.146 ppm2 6.147 ppm2 6.514 ppea 9.456 ppm2 9.122 ppm2 9.118 ppm2 9.119 ppez 4.598 ppm2 | 133 | Wanger | 1 | 1 | 1 |
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and teating	7										
2.000	Peak 1661	0.11000B+01 volume	0.434928+03 ppm1	8.661 ppm2	4.775	188Y	{ 1971} segid "BrD " and	į	•		
and resid 24 and resid 24 000 2.000	4 and name HN))	0.11000E+01 Volume	0.423456.03 pres	4 660	į)) V881	segid *BrD " and resid B4 and 2.600 1.700 peak (1981)	and name HN)) peak 1971 weight	0.11000E+01 volume	0.61276E+03 ppm1	
and resid 24 and resid 24	and name			o o o	484.0	==	segid "BID " and resid 85 segid "BID " and resid 85 2.900 2.100 pc	and name HN)) and name HA)) peak 1901 weight	0.11000E.01 volume	0.32451Ea03 com	
and reeld 2.	peak 1681 and pame	0.11000E+01 volume	0.37096E+03 ppm1	8.654 ppm2	3.089	7 × ×	(1991) segid "BrD " and resid as segid "BrD " and resid as	and but			
and resid 23	3 and name HN }}	0.11000E+01 volume	0.12196E+04 ppm1	8.659 ppm2	9.113	ASS1	3.000	1861 X	0.11000E+01 volume	0.39507E+03 ppm1	
and resid 25 and resid 27 200 1.900	5 and name HN 1) 7 and name HN 1) 0 peak 1711 weight	0.11000E+01 volume	0.817228+02		- *	Yes	2.000 2.000	and name and name peak 2011	0.11000g+61 volume	0.37475R+03 ppm1	
and resid 25 and resid 25 500 2.300	and name and name		0.165200.01)) ((resid as resid as	and name HBI)) peak 2021 weight	0.11000K+01 volume	0.17051E+01 ppm1	
and resid 25 and rand rand 25 and 100 2.000 peak 1	115	0.11000E+01 vol	0.35548.03	rudd see.			resid s6	and name NN)) and name NA)) peak 2011 weight	0.110005.01 volume	0.42952E+03 ppm1	
and resid 25 and resid 25 100 1.700	1 2 5			9.133 DOM2		158	2.000	and name and name peak 2051	0.11000£.01 volume	0.19765E+03 ppm1	
and resid 2:	4 4 1			9.133 bom2	1	Y931	2.100	and name and name peak 2061	0.11000E+01 volume	0.31283E+03 ppm1	
and resid 24 and read 25 and 20 1.400 peak	1771			8.661 Dam2		ABSI	1.700	and name and name Peak 2071	0.11000E+01 volume	0.62404E+03 ppm1	
and resid 24 and resid 24 00 2.200	s and name HW)} s and name HA)} D peak 1791 weight	0.11000E+01 volume		9.196 ppm2		Yes	### ### ### ### ######################	and name and name ak 2001	0.11000E+01 volume	0.28244E+03 ppm1	
and resid 27 and and send resid 26 and 100 peak	7 and name HN)) 6 and name HB1)) 9 peak 1801 weight	0.11000E+01 volume	3	6.169 pro-		A8SI (and name and name ak 2091	0.11000E+01 volume	0.28579E+03 ppm1	
and resid 27 and resid 27 00 1.800 2	\$ \$ \$	0.11000E.01 volume	9) 188V	megid "BrD" and resid 67 megid "BrD" and resid 67 2.700 1.800 1.800 [2111]	and name MN 1) and name MB2 }} isk 2101 weight	0.11000K+01 volume	0.46735R+03 ppm1	
and resid 27 and resid 27 00 1.600 p	334	0.110008+01 VOlume			60.	Yesr (2.200	and hame HN)) and hame HDs) peak 2111 weight	0.11000£+01 volume	0.15320E+03 ppm1	
and resid 27 and resid 26 00 1.700 p	and name and name	0.11000£+01 volume	0.566818403 from	2.1/0 ppm2) ISV	2.400	and name HN)) and name HA)) peak 2121 weight	0.11000£+01 volume	0.22276K+03 ppm1	
2.2	and name and name peak 1851	0.11000E+01 volume				Yes:	1.600	and name HN }} and name HB1 }} peak 2131 weight	0.11000K+01 volume	0.72297£+03 ppm1	
and resid 19 and read resid 19 and r	334			and and an		, ((aid 89 2.200	and name HM 1) and name HA 1} peak 2151 weight	0.11500E+01 volume	0.26347E+03 ppm1	
and resid 20 and resid 19 00 2.000	and name and name	0.00001		9.189 ppm2) Y881	nesid as	and name KN !) and name KB1 !) peak 2161 weight	0.11000E+01 volume	0.26996E+03 ppm1	
and resid 53 and real 63 and resid 63 and r	and name and name yeak 1901	0.11000E+01 volume	0.35792E+03 com1	0.146 ppm2	9.170	(1.400	and name NN)) and name NB2)) peak 2171 Weight	0.11000E+01 volume	0.10141E+04 ppm1	
and resid 63 and and resid 63 and 00 1.600 peak	and name and name peak 1911	G.11000E+01 VOlume					segid "BrD " and resid os segid "BrD " and resid os 2.600 1.700 1.700	and name HN)} and name HN)} peak 2191 weight	0.11000E+01 volume	0.624888.03 ppm1	
and resid 83 and resid 83 00 2.200	354	0.11000E+01 volume	: 6) (• • · · · · · · · · · · · · · · · · ·	2.000	name HN)) name HN)) 2201 weight	0.110008+01 Volume	0.38079E+03 ppm1	_
and resid 64 and resid 64 00 2.000	334	0.11000E+01 volume	: 5			((• 3 AS81 {	resid 46 resid 46 1.800	name HN)) name HA)) 2211 weight	0.11000E+61 volume	0.49246E+03 ppm1	-
and resid 84 and resid 84 00 2.000	334	0.11000E+01 volume	0.42690E+03 ppm1	7.463 ppm2	4, 901	ASSI C	and resid 46 and resid 46 600 1.600	name HN)) name HB1) 2221 weight	0.11000K-01 volume	0.82312E+03 ppm1	-
and resid 84 and resid 84 00 2.200	i and name HN)) i and name HS2)) peak 1951 weight	0.11000K+01 volume		9.463 Dam2		A881 (6	reeld 46	name HB2)) 2331 weight	0.11000£+01 volume	0.72605E+03 ppm1	•
			•		,		eegid "BrD " and resid 47	and name HN))			

| 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 |

3.536

.356 ppm2

1.354 ppm2

5.631

3

. 858

1.671

Ppm2

8.85

3.50

1.656 ppm2

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.355 ppm2

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PPm2

562

1.125

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2

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. 643

. 595

1.355 ppm2

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ppm2

. \$70

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1.572 ppm2

3.014

8.572 ppm2

0.6

2.607

1.571 ppm2

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1.423 ppm2

9.450

.63

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3.919

7.516 ppm2

7.49.7

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1.91		4.571				.380	98.		3.16			9.157		•	• . 475	.7	11.1	2.037	1.031	181.0	7.286
6.375 ppm2	6.679 ppm2	4.678 ppm2	6.670 ppm2	1	0.669 ppm2	1.156 pp. 1.		9	6.695 pos.2	:		See plant			Canada Cal	7900	/ P40 ppm2	Cardo Die.	7. 640 ppm2	7.640 ppm2	6.981 ppm2
0.299\$7E+03 ppm1	0.260238+03 ppm1	0.10062E.04 ppm1	0.20185E+03 ppm1	0.37743E.03 ppm.1	ş	0.34743E+03 ppm1 0.52631E+03 ppm3	8		0.72768E+03 ppm1	0.183316.03 0003		, ecc. 60.88.03	3					3 2	9		0.26366E-03 ppm1
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2521	100	and name and name and name	rent 4351 weight and name NN 1) end name HB2 1) Peak 2561 weight	1 1 2	peak 2551 waight and name HN)) peak 2551 waight and name HN))	name HN)) 2611 weight	Name HN)) Name HA)) M641 waight	Lame HB2))	tabe KM)) tabe HB1)) 1661 weight	tame HH 1) tame HG2 1) 1671 weight	Anne KN)) Anne KK))	name KN)) name KA)) 2731 weight	and name NN)) and name NN)) ask 2731 weight	and name HN)) and name HN)) bak 2751 weight	name HN))	781 44 57	Ame HB))	name KN)) name KG1%) 2801 weight	name HN)) name HG24) 2011 weight	name HW))	peak 3821 weight 0
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478.03		0.427928-01 pres							Catalogue pour	0.19915E-04 pom1	0.462398+03 ppm3	0.100218+03 prm1	235228.03	0.31864R+03 pres1	100,000	0.121668.03 pres		0.63487£+03 ppm1	0.21276E+03 ppm1	0.12947E+03 ppm1	0.201038+03 ppm1	0.54229E+03 ppm1	0.36659E+03 ppm1
ot wollow to	11000E+01 volume 0.144		an lox	,			_																
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and name peak 3431	and name and name peak 3441	and name and name peak 3451	and name and name	and name and name peak 3471	and name and name peak 1491	and name and name	and name and name	and name and name Deak 3521	and name and name peak 3541	and name and name yeak 3562	and name and name seak 1571	and name and name peak 1581	7 P	A 20 1 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1	and name and name peak 3621	7 P P P P P P P P P P P P P P P P P P P	and name and name peak 1651	and name HN and name HGI peak 3651 wei	and name and name peak 3681	and name HN and name HG1 peak 1691 wei	and name and name peak 3701	and name and name peak 1711	and name and name peak 3721
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((segid "BrD " and resid S\$ and name HN	3.295	7.739 ppm2	0.351882+03 ppm1			i
aegid "BrD " and resid 49 and name 3.700 3.400 1.800 peak 4511 (4521)					and resid 32 and name NN))	Ore prise)
2.900 2.100 2.100 po (4511)	3.555	8.627 ppm2	.47519E+03 ppm1	1.11000E+01 volume 0	and resid 60 and name HW)) and resid 67 and name HB1))	((segid BrD ((segid BrD 2 700 1
eegid "BTD" and resid 49 and name 2.600 1.700 1.700 peak 4491 (4501) 4501 and resid 50 and name	4.533	6.480 ppm2	0.10932E-03 ppm3	.11000E+01 volume 0	and resid 11 and name HN)) and resid 10 and name HB2)) .100 2.000 peak 4241 weight c	((megid "BrD (megid "BrD) 3.500 3
segid "BTD" and resid 48 and name 3.200 2.600 2.300 peak 4481 (4491) segid "BTD" and resid 50 and name	4.941	6.480 ppm2	.23699E+03 ppm1).11500E+61 volume 0	and resid 31 and name HN }} and resid 30 and name HS1 }} .300 2.300 peak 4231 weight	((pegid "BrD ((pegid "BrD).000 2
wegid "BrD" and resid 40 and name 4.000 4.000 1.500 peak 4471 4461] 4691d "BrD" and resid 49 and hama	5,449	6.481 ppm2	.86531£+02 ppm1).11000E+01 volume 0	and resid 31 and name HM)) and resid 30 and name HA)) .200 1.500 peak 4221 weight 6	((megid *BrD ((megid *BrD).600 3 ASSI (4233)
aegid BrD and resid 48 and name 1.000 3.200 2.200 peak 4461 4471) and resid 49 and name	3.024	12.275 ppm2	.86536E+02 ppm1	0.11000E+01 volume 0	ceid 30 and name HN)) ceid 29 and name HG1)) 1.900 peak 4211 weight	((***********************************
Pask 4451	2.710	12.275 ppm2	0.11541E+03 ppm1	0.11000E+01 volume 0	esid 10 and name KN)) meid 29 and name KB1.)) 3.100 peak 4201 weight	((eegid *BrD ((segid *BrD 3.400 2
segid "BrD " and resid 46 and 3.100 2.400 2.400 peak (4431) segid "BrD " and resid 48 and	4.619	12.275 ppm2	0.88464E+02 ppm1	0.11000E-01 volume 0	meid 10 and name HN)) meid 29 and name HA)) 1.900 peak 4191 weight	((megid "BrD ((megid "BrD 3.600 3
eegid BrD and resid 46 and 3.500 peak (4441) end zeeld 47 and eegid BrD and zeeld 47 and	3.406	9.152 ppm2	0.65813E+02 ppm1	0.11000£+01 volume 0	meid 29 and name HB3)) meid 28 and name HB3)) 1.700 peak 4181 weight	((megid "BrD ((megid "BrD 3.600]
segid "BrD " and resid 46 and 1,300 2,700 2,200 peak (41) 9431}	3.597	9.151 ppm2	0.11906E+03 ppm1	0.11000E-01 volume 0	ceid 29 and name HN) ceid 26 and name HB1)) 2.100 peak 4171 weight	((megid "BrD ((megid "BrD 3.400 2 ASSI (4181)
aegid "BrD" and resid 34 2.600 2.000 2.000 pe { 4421} eegid "BrD" and resid 47	4.574	9.151 ppm2	0.91502E+03 ppm1	0.11000E+01 volume 0	meid 29 and name NM)) meid 26 and name NA)) 1.400 peak 4161 weight	((megid *BrD ((megid *BrD 2.400 1
segid "BrD " and resid 42 and 2.500 2.100 2.100 peak [4411] 8PD " and resid 34 and segid "BrD " and resid 34 and	\$.055	8.166 ppm2	0.14739E+03 ppm1	0.11000E+01 volume o	meid 28 and name HN }) seid 27 and name HA }) 2.200 peak 4151 weight	((megid "BrD ((megid "BrD 3.300 2
ampid "BrD " and resid 42 and 2.800 2.000 2.000 peak [4401] and resid 41 and	4.493	8.171 ppm2	0.184915+03 ppm1	0.11000K+01 volume 6	meid 27 and name HN 1) meid 26 and name HA 1) 2.300 peak 4141 weight	((eegid 'BrD (eegid 'BrD).200 2
eegid "BrD " and resid 42 and 2.900 2.100 2.100 peak (4.91) eegid "BrD " and resid 41 and	950.5	9.131 ppm2	0.87462E+03 ppm3	0.11000E+01 volume (esid 25 and name HN)) esid 24 and name HG2)) 1.600 peak 4121 weight	((megid "BrD ((megid "BrD 2.500 1
aegad "BrD " and resid 38 and 3.100 2.400 2.400 peak { 4.31} eagled "BrD " and resid 43 and	4.753	9.133 ppm2	0.14843£+03 ppm1	0.11000E+01 volume (esid 25 and name HW)) msid 24 and name HA)) 2.200 peak 4111 weight	((megid 'BrD ((megid 'BrD) 100 AESI (4121)
1.900 peak 1.900 peak	6.640	8.661 ppm2	0.11008R+03 ppm1	0.11000E+01 volume (meid 24 and name HN 1) ceid 23 and name HA 1) 2.000 peak 4101 weight	((megid 'BrD ((megid 'BrD 3.500)
segid "BrD " and resid 30 and 3.400 2.800 2.100 peak [4.451] end resid 39 and segid "BrD " and resid 39 and	4.734	9.116 ppm2	0.91130K+02 ppm1	0.11000K+01 volume (and resid 23 and name NM)) and resid 22 and name NA)) .200 1.900 peak 4091 weight	((megid 'BrD ((megid 'BrD 3.600)
((equid 'Bro' and reads 20 and name 2.300 1.300 1.300 peak 431) (eduid 'Bro' and reads 2.300 (eduid 'Bro' and reads 2.300 eduid 'Bro' and 'Bro' and 'Bro' and 'Bro' and	4.34	9.457 ppm2	0.15236E.03 ppm1	0.11000E+01 volume	and resid 22 and name NN]) And resid 21 and name HA]) 700 2.200 peak 4081 weight	((eegid 'BrO ((eegid 'BrO) 100 2
### ### ### ### ### ### ### ### #### ####	4. 65	8.545 ppm2	0.11425E+03 ppm1	0.11000K+01 volume (esid 21 and name HN)) esid 20 and name HA)) 2.100 peak 4071 weight	((megid 'BrD ((megid 'BrD 3.400 ABBI (4081)
eegid "8rD " and resid 35 3.300 2.700 2.200 pe { 4321}	4.288	1.146 ppm2	0.17148E+03 ppm1	0.110008+01 volume	and resid 20 and name HN)) and resid 19 and name HA)) .600, 2.300 peak 4061 weight	((eegid BrD ((eegid BrD) 200 3
megid "BrD " and resid 17 and 1.500 1.100 2.000 peak (4.111) eegid "BrD " and resid 16 and	3.478	9.167 ppe2	0.95460E+02 ppm]	0.11000E+01 volume	esid 19 and name HN)) esid 18 and name HA)) 2.000 peak 4051 weight	((eegid 'BrD ((eegid 'BrD).500
1	9.062	6.669 ppm2	0.57514E+03 ppm1	0.110008+01 volume	reald 17 and name HW)) (maid 18 and name HW)) 1.700 peak 4041 weight	((segid "BrD - and i ((segid "BrD - and i 2.600 1.700
aegid 'BrD " and resid 11 2.300 1.300 1.300 (4291)	1,749	9.073 ppm2	0.33212E-03 ppm1	0.11000E-01 volume	resid 18 and name HN)) resid 17 and name MG24) 2.400 peak 4021 weight	(eegid 'BrD { eegid 'BrD 3,100 A881 { 4041}
{ 4271} megid "BrD" and resid 32 and	4.511	9.072 ppm2	0.187248+63 ppm1			

7.739 ppm2

0.11000E+01 volume 0.11812E+04 ppm1

5.537

7.734 ppm2

0.17960E-03 ppm1

0.11000E.01 volume

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8.309 ppm2

0.110005+01 volume 0.97101E+02 ppm1

. 133

0.306 ppm2

0.110005-01 volume 0.16106E-01 ppm1

3.458

6.307 ppm2 9.652 ppm2

0.11000E+01 volume 0.7855E+02 ppm1

0.11000K+01 volume 0.15683E+04 ppm1

1.752

9.652 ppm2

0.11000E+01 volume 0.11939E+03 ppm1

\$.055

8.001 ppm2

0.11000E+01 volume 0.31481E+03 ppm1

2.761

8.001 ppm2

0.11000E+01 volume 0.36989E+03 ppml

0.001 ppm2

0.32280E+03 ppm1

0.11000E+01 volume

0,776

9.652 ppm2

0.11000E+01 volume 0.20061E+01 ppm1

1.071

9.652 ppm2

0.11000E+01 volume 0.93234E+02 ppm1

4.119

4.632 ppm2

0.11400E+01 volume 0.14320E+03 ppm1

2.638

6.306 ppm2

0.11000E+01 volume 0.42122E+03 ppm1

3.296

8.832 ppm2

0.110008+01 volume 0.110118+03 ppm1

1.094

4.433 ppm2

0.11000E+01 volume 0.20297E+03 ppm1

8.307 ppm2

0.110008+01 volume 0.168495+03 ppm1

1.116

7.762 ppm2

0.11000E+01 volume 0.24376E+03 ppm1

2.472

7.762 ppm2

0.11000E.01 volume 0.45441E.02 ppml

0.11000E+01 volume 0.17937E+03 ppm1

2.693

.63

6.564 ppm2

0.11000E.01 volume 0.60014E.01 ppm1

2.622

1.564 ppm2

0.110008+01 volume 0.31627E+01 ppm1

1.564 ppm2

0.11000E+01 volume 0.77577E+02 ppm1

9. 262 99	6.75 pp	6.763 po		6.427 pp	. 626	. 305 pp	6.304 pue	1.306 pos					. 040	dd 540 3						4.611 ppm	7.986 ppm2	7.994 ppm2
0.48168E+03 ppm1	0.11537£+03 ppm1	0.13653E+03 ppm3	0.41855E+03 ppm1	0.12732£+03 ppm1	0.15213E+03 ppm1	0.958158.03 ppm1	0.22391E+03 ppm1	0.15981E+03 ppm1	0.24443E+03 press					0.104308.03	į į	į į		, <u>1</u>		0.59739E-03 ppm1	15554E+03 ppm1 7	0.86259E.03 ppm1 7
0.11000E-01 volume 0	0.11500E+01 volume (0.11000£+01 volume 0	0.11000E.01 volume 0	0.11000£+01 volume 0	0.11000E+01 volume o	0.11000E+01 volume 0	0.11000E.01 volume 0	0.11GDOE+01 volume 0	0.11000E+01 volume 0					volume		volume	0.11000E+01 volume 0.	0.11000E+01 Volume 0.	0.11000E+01 volume 0.	0.110008+01 volume 0.	0.11660E+01 Volume 0.3	0.11000E+01 volume 0.6
66 and name KN)) 65 and name KA)) 800 peak 4801 weight	3 3 4	ššį	67 and name HW 1) 64 and name KA 1) 100 peak 4831 weight	and name NN }} and name HA }} meak 4841 weight	67 and name MM)) 67 and name MM2)) 100 peak 4851 weight	resid 68 and name MM)) resid 68 and name HA)) 1.400 pesk 4861 meight	and name HN 1) and name HB1)) max 4071 weight	resid 69 and name NB)) resid 68 and name NB2)) 2.200 peak 4881 weight	and name HN)) and name HA)) ak 4891 weight	and name HN }) and name HB }) ak 4901 weight	and name HM:)) and name HGIS) ak 4911 weight	and name HM)) and name MG24) wak 4921 weight	and name HN 1) and name HA 1) mak 4931 weight	and name KM)) and name KA)) peak 4941 weight	and name KN)) and name KA)) peak 4951 weight	and name HN)) and name HA)) peak 4961 weight	and name HN)) and name HO1)) peak 4971 weight	and name HN)) and name HG2)) peak 4981 weight	and name HW)) and name HB2)) meak 4991 weight	and name HN)) and name HB1)) mak 5001 weight	and name HM)) and name HA)) seak 5011 weight	and name HM)) and name HBW) pask \$021 weight and name HW))
[4801] eegid 'BrD' and resid 66 eegid 'BrD' and resid 65 2.700 1.800 1.800 [eegid 'BrD - and resid 66 eegid 'BrD - and resid 65 3.400 2.900 2.100	aegid "BrD " and resid 66 eegid "BrD " and resid 65 3.300 2.700 2.200 [4631]	emgid "BrD" and resid 67 emgid "BrD" and resid 66 2.000 3.000 2.000 p	segid "BrD " and resid 69 segid "BrD " and resid 67 3.400 2.900 2.100 g	egid "BrD " and resid 68 egid "BrD " and resid 67 .300 2.700 2.200 4861)	eegid 'BrD ' and resid eegid 'BrD ' and resid 2.400 1.400 1.4	(segid 'BrD " and resid 69 (segid 'BrD " and resid 68 4.500 4.500 1.000 p	seyid "BrD" and resid seyid "BrD" and resid 3.300 2.700 2.31	segid "BrD " and resid 70 segid "BrD " and resid 69, 3.000 2.200 2.200	(eegid "BrD " and reaid 70 (eegid "BrD " and reaid 69 3.400 4.500 7.500 pg (4.500)	segid "BrD" and resid 70 segid "BrD" and resid 69 1.700 f	ugid "BrD" and resid 70 ggid "BrD" and resid 69 700 1.800 1.800 p	4931) gad "BrD " and resid 73 gid "BrD " and resid 72 9900 2.100	4941) gid "BrD" and resid 74 gid "BrD" and resid 73 500 3.000	eegid "BrD" and resid 75 seegid "BrD" and resid 74 3.500 3.100 2.000	megid BrD and resid 7s aegid BrD and resid 7s 3.400 2.900 2.100 [second "BrD" and resid 76 second "BrD" and resid 75 3.000 2.200 2.200	(aegid "BrD " and resid 76 (aegid "BrD " and resid 75 1.200 2.600 2.300 [4991]	eegid "BrD " and resid 76 eegid "BrD " and resid 75 2.600 1.700 1.700	megid."Brp " and reaid 76 aegid "Brb " and reaid 75 1.600 1.700 p. [5011]		14d BrD and resid 77 24d BrD and resid 76 500 1.600 1.600 14d BrD and resid 79
. ASSI (A861 (((e	(1 e	((e)) ((A881	1 1 4 10 K					- I n	A881	A661 (1 1004		((pp. () pp.	(ee	((meg ((meg 2.4	188Y	NE
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7.974 ppm2	7. 875 ppm2	pudd start		radd	s. 35 a ppms	Tu. 050 ppm	rudd	5.49e ppm2	6.496 ppm2	10.051 ppm2	6.743 ppea	6.743 ppm2	6.749 ppm2	8.566 ppm2	8.997 ppm2	9.477 ppm2	9.472 ppm2	8.206 ppm2	7.576 ppm2		7.634 ppm2	7.513 ppm2
	0.20373E+03 ppm1										ē	0.728765+03 ppm1	0.14220K+03 ppm1						0.17538E-03 of-e1			0.90206E+02 ppm1
0.11000E+01 volume			0.11000E+01 volume					?	•						vol une	volume	ğ		am fox	volume		0.11000E+01 volume

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6.683 pom2		7.996 ppm2	8.006 ppm2	0.006 ppm2	8.006 ppm2	7.619 ppm2	6.981 ppm2	6.981 ppm2	. 6KB	660 Dam	9.658 ppm3	:		9.463 ppm2	9.463 ppm2	7.515 ppm2	7.516 ppm2	8. 623 ppm2	572 ppm2	.357 ppm2	6.354 ppm2	1.354 ppm2	1.355 ppm2
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0.14	•			0.15	0.164		0.01066	0.121	0.113	0.107	0.413	0.19					0.12439		•	P.87457E+03	0.234568+03	0.19424E+03	0.676
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HA))	== }		EE A									HN)) HB)) weight o											
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HB123) HB1 }}

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1.875 ppm2

7.00

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2.703

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9.042 1.764

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1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 1511 | 15

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674 ppm2 6.674 ppm2

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0.47200E+03 ppm]

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9.155 ppm2

0.000086+03 ppm

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9.187 ppm2

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0.20903&-03 ppm1	.66916E+02 ppm1	.67760£+03 ppm1	0.162888+02 ppm1	0.7\$253&+03 ppm1	0.765955+02 ppm1	0.785926+03 ppm1	0.675108.02 ppm1	0.147018+04 ppm1	0.10\$77£+01 ppm1	0.39234E+02 ppm1	0.85958E+02 ppm1	0.51430E+03 ppm1	0.21373E+02 ppm1	0.17364\$+03 ppm1	0.236568+03 ppm1			0.37426E+03 ppm1	0.22483K+03 ppm1	0.56508E+02 ppm1	0.57592E+03 ppm1	0.30043E+01 ppm1	
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99.0 0.793

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0.61252E+00 ppm1

HD24) Weight 0.11000E+01 volume

8.014 ppm2

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volume volume 4.445

6.423 ppm2

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1.09

6.571 ppm2

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0.105156.03

volume

6.553

6.424 ppm2

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Volume

no resid 61 and name HM 1)

of cesid 64 and name HM 1)

of 2.000 peak loss weight

of resid 87 and name HM 1)

of resid 88 and name HM 1)

of resid 88 and name HM 1)

of resid 88 and name HM 1)

of 1.100 peak loss veight 0

of 2.100 peak loss veight 0

. 445

6.572 ppe2

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volume

7.596

. 45 ppm2

0.19134E-03 ppm1

volume

1.559

6.856 ppm2

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volume

of resid 89 and name HH))
of creid 31 and name HD1))
of C.200 peak 11071 weight of creid 89 and name HH))
of creid 31 and name HD2))
of 1.700 peak 11081 weight of

4.400

6.858 ppm2

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2.779

6.658 ppm2

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d resid 69 and name HH))
d resid 67 and name HB))
1.700 peak 11101 weight of feeld 89 and name HB))
d feeld 87 and name HB))
1.300 peak 11111 weight 0

2.610 0.059

6.865 ppm2

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0.11000E+01 volume

6.676 ppm2

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0.167705.03

volume

1.364

8.680 ppm2

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0.11000E.01

HM 1)

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3.796

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4.182

6.307 ppm2

3.40 5.727

0.307 ppm2 8.832 ppm2 £. \$23

6.377 ppm2

1.995

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1.926

9.003 ppm2

7.944

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1.780

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1. 11

9.004 ppm2

9.93

9.002 ppm2

4.650

7.822 ppm2

1.83

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6.146 ppm2

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	0.669 ppm3	4.669 ppm2			4.513 ppm2		redd 186.	6.960 ppm2		6.980 ppm2	0.522 ppm2		6.218 ppm3	8.218 ppm2	6.355 ppm2	366		1.356 ppm2	8.355 ppm2	8.883 ppm2	6.063 ppm2		8.086 ppm2	6.632 ppm2	6.432 ppe2	:	7. 762 ppm2	9.004 ppm3	;	7. 620 ppm2
	0.47923E+02 ppm1	0.19841E+02 ppm1			0.11136g.03 ppm1	0 142715-01		0.11969K+03 ppm1		0.48486E+03 ppm1	0.202028+00 ppm1		0.28750K+02 ppm1	0.12771E+03 ppm1	0.11613E+03 ppm1	0.47664E.01 pcm;		restored to serve	0.760818+02 ppm1	0.17242E+02 ppm1	0.16590E+03 ppm1	:	0.17496E+03 ppm1	0.33544E+02 ppm1	0.605196+02 pp=1		. superfiction press	0.53690E+02 ppml		
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and name	11	and name and name peak 11721	and name and name peak 13751	and name and name peak 11881	aid 62 and name best of 67 and 13691	eid lis and name i mid 75 and name i 0.500 peak 13931 v			13961	0001	100	eatd 108 and name eatd 110 and name 0.300 peak 14033	14051	resid 106 and name H resid 21 and name H 0.900 peak 14081 v	ne 1	eid 105 and name F eid 103 and name F 0.500 peak 14101 v	resid 100 and name F	0.800 peak 14181 w	1.100 peak 14211 visid by and name beat 101 and name beat 101 and name beat	and name	1959	i 11	
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1.706	2.169	1.63		1.480	1.763	B. 121	3.393	1.493	1.250	1.596	2.803	1.864	1,239	3.213	8.475	7.742		7.944	5. 450	1.967	3,344	1.077	0.743
9															•								4
7.420 ppm2	6.145 ppm3	6.147 ppm2		8.146 ppm2	6.146 ppm2	9.119 ppm2	9.196 ppm2	9.195 ppm2	9.196 ppm2	6.169 ppm2	8.169 ppm2	6.498 ppm2	8.499 ppm2	6.565 ppm2		11.082 ppm2		082 ppm2	11.082 ppm2		0.613 ppm2	9.680 ppm2	9.681 ppm2
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8.794 ppm2

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0.26713E+03

VOLUME

B. 140

7.537 ppm2

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1.562 ppm2

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0.18636E+02

3.557

1.334 ppm2

0.40043E.02 ppm1

volum

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6.086 ppm2

0.121685.02 ppm1

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6.355 ppe2

0.38338E+02 ppm1

1.642

6.375 ppm2

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0.49230E+02

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3.665

4.377 ppm2

0.9997E+01 ppm1

volume

9.745

6.529 ppm2

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volume

3.

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8.521 ppm2

0.951496+01 ppm1

volume

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8.980 ppm2 9.740 ppm2

0.23253E+02 ppm1

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4.467 ppm2

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24

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		0.22594E+02	0.206438+03	0.549698+02	0.813058+02	20.23		0.159318-02 0001	0.45701£+02 ppm1	0.31541E+02 pres	0.212358+02	0.90159E+02 ppm1	0.40125K+02	0.16509E+02	0.189092+02	0.63142E+03 ppm1	0.13744E+02 ppm1	0.161878+03	0.53302\$+02 ppm1	0.211728+0	0.30250 6+0 2 ppm3	0,715596+02 ppml	0.14588R+02
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resid 95 and name resid 32 and name 1.800 peak 14321	esid 93	1.000 1.000	0.800	meid 89 1.600	**************************************	resid as resid at	estd 83 0,700	e 1d 79	esid 39 1.500	resid 76 resid 74 1.200	e 1d 72 e 1d 75	1.900	** id 64 1.400	esid 64 esid 65 0.700	resid 63 resid 74 0.900 pe	resid 62 resid 61 1.700 pe	resid 62 resid 65 1.300 pe	resid 57 resid 35 2.300 pe	resid as resid as 1.600 pe	resid 54 resid 64 0.900 pe	resid 48 resid 46 1.200 pe	reald 48 reald 49 1.800 pe	resid 92 0.600 pe
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10000E+01 volume	0.16000E+01 volume	0.10000E+01 volume	0.10000E.01 volume	0.10000E+01 volume	0.10000E+01 volume	0.10000\$+61 volume		0.10000E+01 volume	0.10000E+01 volume	0.16696E-01 volume		0.10000E+01 volume	0.10000E+01 volume	0.10000E+01 volume	.100005.01 volume	. 10000E-01	volume	volume	0.100008+01 volume (0.10000E.01 volume (0000E+01 volume	. 100008+01 volume 0	0.10000E+01 valume 0
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and name hand hame hand name H	and name and name pack 15551	and name and name peak 15633	and hame and hame	and name	and name	and name and name peak 27072	and name and name peak 26993		and name and name peak 26732		and name and name peak 26823	pus pus	resid 43 and name resid 47 and name 1.600 peak 19122	4 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	p p	* *	Δ.	Δ.	Pe a sh	2 5 5 4 2 5 5 5	and name and name peak 113	2 4 4 5 2 4 4 5	2 4 4 5 E	333	•
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3.635 ppm2

0.11000E+01 volume 0.11498E+04 ppm1

1.21

2.635 ppm2

5.021

2.487 ppm3

0.244825+03 ppm1

0.11000E+01 volume

\$.021

2.433 ppm2

0.368628.03 ppm

0.11000E+01 volume

5.14

4.407 ppm2

0.89203E+03 ppm3

0.11000E+01 volume

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5.11 2.93

4.263 ppm2

5.098 ppm2

0.11000E+01 volume 0.42716E+03 ppm1

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0.11000E+01 volume

4.337

2.631 ppm2

1.337

2.981 ppm2

5.114

2.645 ppm2

0.11000E+01 volume

0.11000E+01 volume

5.114

2.729 ppm2

0.11000E-01 volume 0.14259E-03 ppml

. 153

4.657 ppm2

3.78

2.519 ppm2

3.78

2.598 ppm2

0.11000E+01 volume 0.14619E+03 ppm.

2.346

2.519 ppm2

0.11000E+01 volume

3.598 ppe2

0.80668E+02 ppm1

0.11000E+01 volume

0.11000E.01 volume

2.940

4.403 ppm2

2.851

4.403 ppm2

0.11000E+01 volume 0.10971E+03 ppm1

4.518

1.185 ppm2

1.652

1.154 ppm2

volume VO) LINE

1.651

1.253 ppm2

1.651

2.330 ppm2

0.11000E+01 volume

1.453

3.076 ppm2

0.277158+03 ppm1 0.60399E.02 ppm1

0.1100dE+01 volume

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1.700	resid 78 and resid 78 and 1.300 peak	resid 16 and resid 18 and 1.700 peak	resid 18 and resid 18 and 1.800 peak	resid 16 and resid 16 and 1.700 peak	resid 102 and resid 102 and 1.300 peak	esid 73 and esid 73 and 1.300 peak	esid 73 and esid 73 and 1.400 pesk	esid 73 and esid 73 and 1.600 peak	celd 56 and celd 56 and 1.800 peak	eaid S6 and 2.100 peak	esid S6 and esid S6 and 1.300 peak	esid 22 and esid 22 and 1.600 peak	esid 22 and	seid 22 and	1.200 peak esid 63 and esid 63 and	resid 63 and	resid 66 and resid 66 and	resid 66 and	resid 100 and resid 100 and 1.100 peak	meid 114 and meid 114 and 1.100 peak	esid 85 and esid 85 and 1.800 peak		**************************************
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volume 0.14970£+03 ppm1

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3.451

4.953 ppm2

0.12205E-03 ppm3

0.110005+01 volume

2.776

4.952 ppm2

0.14430E+03 ppm1

0.11000E+01 volume

2.657

4.457 ppm2

0.11000E+01 volume 0.2143E+03 ppm

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4.457 ppm2

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0.11000E+01 volume

0.11000E+01 volume

1.13

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4.637

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4.582

4.902 ppm2

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2.360

4.410 ppm2

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0.11000E+01 volume

3.206

4.409 ppm2

1.715

4.408 ppm2

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0.11000E-01 volume

1.661

4.408 ppm2

0.14800E+03 ppm1

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0.110002+01

1.261

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4.407

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0.22343E+03 ppm1

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4.952 ppm2

0.11000K+01 volume 0.12930K+03 ppm1

4.671

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and name [11] and name [12] an	0.917
and name [11] and name [12] an	_
and name HE 1) and name HE 1 1 and name HE 2 1 and name HE 2 1 and name HE 2 1 and name HE 3	5 ppm2
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and mass (M.) 19 and ma	0.15454K+03
and name HRI	
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2.100 1.700	2.600 (8462) 8491d 'BrU
	2. 400 - 4462)
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1.320	4.398	15		4.63	5	0.767	2.101						. 520				1.07	1.63	1.743	3.634	.443	4.434	1.760
0.416 ppm2	2.62 pp.	2.386 ppm2	. 704 204 204	1.544 ppm2	1.35	1.254 ppm2	4.80\$ ppm2	1.84	3.967 pomp	1.307 Press		Tale of the second	add cor :	1.254 ppm2	0.761 8082	0.662	0.662 ppm2	0.663 pps	4.343 ppm3	4.263 ppm2	1.333 ppm2	1.303 ppm2	1.363 ppm2
0.23426£+01 ppm1	0.27789E+03 ppm1	0.10282E+03 ppm1	0.254848+03 ppm1	0.34485E+03 ppm1	0.147795.03 ppm1	0.48347E+03 ppm1	0.22156E+03 ppm1	0.42630E+03 ppm1	0.670028+02 ppm1	0.75592E+02 ppm1	0.132448.03 press			0.25176K+03 ppm1	0.139378+03 ppm1		0.17974E+03 ppm1	0.24075E+03 ppm1	0.18319E+03 ppm1	3.21483E+03 ppm1).141448+03 ppm1).20447E+03 ppm1	11841E+03 ppm1
0.11000E-01 volume	0.11000E+01 volume	0.11000E-01 volume	0.11500E.01 volume	0.11000E+D1 volume	0.11000£.01 volume	0.11000E+01 volume	0.11000K+01 volume	0.11000E; 01 volume	0.11000E+01 volume	110005-01 volume	.11000£+01 volume	0.11000E+01 volume		1.11000£+01 volume	1.11000E+01 volume (1.11006E+01 volume (0.11000E+01 volume (0.11600£+01 volume (0.11600E.01 volume 6	.11000E+01 volume 0	0.11000E+01 volume 0	.11006E-01 volume 0	.11000E.01 volume 0
id 102 and name HD21) 0.000 peak 8462 weight	2 and name HB1 1) 9 and name HA 1) 0 peak 8552 weight	2 and name MB2 2 and name MD14 0 peak 8562 weight	2 and name HA)) 5 and name HB)) 0 peak 8602 weight	6 and name HD10) 6 and name HA)} 0 peak 8652 weight	6 and name HD14) 8 and name HD14) 0 peak 8672 weight	and name HD24) and name HD34) peak 8682 weight	and name HA)) 6 and name HBA) 9 peak 8722 weight	and name HD11) and name HB1)) peak 0742 weight	and name KA)) and name KEs) peak 8752 wasght	s and name HB1)) and name HB4) peak 6782 weight	sid 78 and name MB2) eld 59 and name HEN) 2.100 peak 8792 weight (and name KB1)) and name KA)) pask 8802 weight	and name MG 1) and name HEt)	and Pass and and Pass and and Pass and Pass and Pass and Pass and Pass and Pass and Pass and Pass and and Pass and and Pass and and and and and and and and and and	and name KD14) and name NEt) peak 8652 weight	and name HD21) and name HO21) peak 8872 weight (and name MD24) and name MD14) peak 8892 weight	name HD24) name HE4) 8912 weight	Same KA 1) Some MB1 1) 1922 veight	2 and name HA)) 5 and name HB2)) peak 8932 weight o	and name HB1)) and name HA)) eak. 8952 weight	and name and name ak 1972	2 and name MD14) 6 And name MB1) pask 6962 weight 0
	12 mg1d "BrD" and reald 22 mg1d "BrD" and reald 19 mg1d 19 mg1	1914 'BrD ' and resid 32 1914 'BrD ' and resid 22 500 1.600 1.600	1914 BrD and resid 23 1914 BrD and resid 25 1600 1.700 1.700	mgid "BrD * and reald 56 mgid "BrD * and reald 56 500 1.600 1.600	1914 "BrD " and resid \$6 1914 "BrD " and resid 78 900 2:100 2:100	1914 "BrD " and resid 56 1914 "BrD " and resid 78 100 1.300 1.300	gid 'BrD " and resid 71 gid 'BrD " and resid 76 700 1.800 1.800	9id "BrD " and resid 73 9id "BrD " and resid 73 400 1.400 1.400	"gid "BrD " and resid 78 "gid "BrD " and resid 59 3300 2,700 2,200	gid BrD and resid 78 gid BrD and resid 59 2.300 2.300	rD • and re rD • and re 2.100	2 2	: :	9822} 91d BrD sed resid 76 91d BrD sed resid 81 600 1.700 1.700	gid "BrD" and resid 7e gid "BrD" and resid 59 900 2.100 2.100	gid "BrD" and resid 78 gid "BrD" and resid 25 600 1.700 1.700	1914 "BrD " and resid 78 1914 "BrD " and resid 81 800 2.000 2.000 pe	91d 'BrD' and resid 78 a 91d 'BrD' and resid 59 a 600 1.700 1.700 pee	31d 'BrD " and resid 102 and 1 31d 'BrD " and resid 105 and 1 100 2.000 2.000 peak (## BrD * and reald 102 and 103	3id "BrD" and resid 102 3id "BrD" and resid 99 800 2.100 2.100 p	31d "BrD" and resid 102 31d "BrD" and resid 25 300 1.800 1.800 p	14 "BrD" and resid 102 144 "BrD" and resid 108 100 2.300 3.200
, se 5.	-51 E	- 8 8 4-	Y 25 25	. 1 1 4-	- 1 1 4 -	ASS1 ~ .	(98 (98 7.2.	- 2 2 4 -	- 1 1 4 -	- 8 8	- 2 2 4 -	- 1 1 1	-11.	A891	- 1 1 4-	- 11	- 2 2 4	ASSI 2.0	ABI :: .	((asg () asg 3.7	5) 1597 5))	ABSI (e	

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E+01 volume 0.1325E+03 ppml	E-01 volume 0.16112E-03 ppm1	E+01 volume 0.157618+03 ppm1	E-01 volume 0.15186E-03 ppm1	E-01 volume 0.11074E-03 ppm1	volume 0.16684E+03	volume	volume 0.17054E+03	01 volume 0.21944E+00	volume 0.23373E-02	E-01 volume 0.23785E+03 ppm1	E+01 volume 0.14616E+03 ppm1	Volume 0.13342E+03		6-01 Volume 0.519226-02 ppm:	E-01 volume 0.10268E-03 ppm1	8-01 volume 0.660878+02 ppm:	E-01 valume 0.77164E-01 ppm1	6-01 volume 0.675955-01 pps1	e de la contraction de la cont		1+01 volume 0.15716E+03 ppm1	1+01 volume 0.13922E+01 ppm.1	1.01 Volume 0.37492E+03 ppm1	0.11000E+01 volume 0.48547E+03 pps; 0.11000E+01 volume 0.37381E+03 pps;
name MB2))	name HA) teame HB1) 9612 weight 0.11000g		Name KA)) Name KB2)) 9832 weight 0.11000E+01	name HDI)} 9862 weight 0.11000E+01	name HB2 }) name MA }} 9872 weight 0.11000E+01	name HB1)) name HA)) 9912 weight 0.110006-01		name HB1 }} name HD1 }} 9932 weight 0.11000£.	name NB2 }] name ND1 }) 9942 weight 0.11000&+01	name HG1 }) name HD1 }) 9952 weight G.11000E+01	name HB1 } name HA }} 9962 weight 0.11000E+01	name HB2)) name HO1)) 9982 weight 0.110006+01	191	Ame HA))	062 weight 0.11000\$+01	44mc HB1 }} 072 weight 0.110008.01	name KU1 } name BO24) 10112 weight 0.11000E+01	ame HG2%) ame HG3%) 122 weight 0.110006+01	ADD (82)) ADD (821) 132 WEIGHT 0.11000E.01		232 weight 0.110008+03 ease MB2)) ease MA))	242 weight 0.11000E-01	252 weight 0.11000E-01	# 12 # 12 # 12 # 12 # 12 # 12 # 12 # 12
eegid "BrD " and resid 101 and 2.900 2.100 2.100 peak [9812]	1991 815 and resid 103 and 2.800 2.000 peak	aegid "BID" and resid 103 and aegid "BID" and resid 106 and 3.800 2.000 2.000 peak { 9812}	segid "BrD " and resid 103 and segid "BrD " and resid 106 and 2.800 2.000 2.000 peak [962]	segid 'BrD ' and resid 10 and segid 'BrD ' and resid 11 and 1.000 2.200 2.200 peak	segid 'BrD' and resid 22 and segid 'BrD' and resid 19 and 2.000 2.000 peak	segid 'BrD' and resid 16 and segid 'BrD' and resid 16 and 2.700 1.800 1.800 peak	9922 segid BrD and resid 16 and segid BrD and resid 16 and 1.000 2.000 peak	megid "BrD" and resid 36 and segid "BrD" and resid 37 and 5.500 5.500 0.000 peak	1 9944 BrD and resid 16 and eegid BrD and resid 17 and 1990 1,500 1,600 peak	segid "BrD " and resid 16 and segid "BrD " and resid 17 and 2.600 1.700 1.700 peak [9623	segid BrD and resid 54 and segid BrD and resid 54 and 2.90 2.100 2.100 peak	eegid BrD and resid 54 and segid BrD and resid 54 and 2.900 2.100 2.100 peak	(10042) eegid "BID" and resid 54 and hame eegid "BID" and resid 54 and name 3.400 2.500 2.500 mask inaxy	(10062) segid 'BrD * and resid 35 segid 'BrD * and resid 35	3.000 2.300 2.300 {10072} segid BrD and resid 35	96910 87D and resid 15 and 1.100 2.400 peak 10112	action of the control	segid 'BrD' and resid 70 and name segid 'BrD' and resid 69 and name 4.800 4.800 0.700 peak 10122	(10112) section 2.600 and name section and name section and resid 89 and name 3.200 2.600 2.600 peak 10112	(10232) segid 'brD * and resid 7 segid 'BrD * and resid 7	1.800 2.000 2.000 (10242) eegid *BrD * and resid 7 segid *BrD * and resid 7	2.900 2.100 2.100 [10252] eegid "BrD" and resid 42 secid "BrD" and resid 42	2.400 1.400 1.400 (1.400 pogid 42	2.300 1.300 (10312) 4-91d 'BrD ' and megid 'BrD ' and 2.400 1.400
) ASS	Yes		,		33		A58A				3 554			A681	1054	A 68	ASS		Asset C.	788 Y	1987 ((183 8	2	AS8
3.6					3.074		0.410	3.883	0.834	3.820	2.500	1.2.1	4.690	2.302	4.810	1.807		4.610	1.651	1.976	2.949	2.657	2.930	4.775
1.303 ppm2			redd for r	3.190 ppm2	4.360 ppm2	2.488 ppm2	1.201 ppm2	1.205 ppm2	1.397 ppm2	1.006 ppm2	1.006 ppm2	1.004 ppm2	1.008 ppm2	4.265 ppm2	2.533 ppm2	3.444 ppm2	:	1.547 ppm2	4.411 ppm2	4.411 ppm2	4.784 ppm2	4.653 ppm2	4.653 ppm2	2.733 ppm2
0.169568+03 ppm1	0.27744£+03 ppm1			0,56334E+03 ppm1	0.11815E+03 ppm1	0.162188+03 ppm1	0.131318+03 ppm1	0.13713E+03 ppm1	0.31566R+03 ppm1	0.224498+03 ppm1	0.954318+02 ppm1	0.16689E+03 ppml	0.33859E+03 ppm1	0.11803E+03 ppm1	0.31366E+03 ppm1	0.48978+03 pm1		0.26958R+03 ppm1	0.11168E+03 ppm1	0.203838+03 ppm1	0.10771E+03 ppm1	0.47366E+03 ppm1	0,386298+03 ppm1	0.14088E+03 ppm1
0.11000E+01 volume	0.11000E-01 volume	: 5		0.11000£•01 volume	0.11000£+51 volume	0.11000£+01 volume	0.11000£+01 volume	0.11000E+01 volume	0.11000E+01 volume		0.11000£+01 volume	0.11000E+01 volume	0.11000E.01 volume	0.11000E+01 volume	0.11000E.01 volume	0.11000E+01 volume		d.11000E+01 volume	0.11000K+01 volume	0.110008.01 volume	0.11000E+01 volume	0.11000E+01 volume	0.11000E+01 volume	0.1100DR.01 volume
2 and hame HD14) 5 and hame HB2); peak 8992 weight	2 and name MD14) and name MB1 }} peak 9002 weight	9 9 5	200	Neme Traine	pack 9082 and name	peak 9092 and name and name	peak 9182 and name	peak 9222 and name and name	and name	peak \$292 and name and name	peak 9302 and name and name	peak 9312 and name and name	322	100	12	1 and name HG11)) and name HG12)) peak 9372 weight			432	3	and name peak 9712	and name HB2	and name and name ak 9772	and name HB1) and name NA) peak 9762 weight and name NA)
"BrD " and resid 102 and name "BrD " and resid 105 and name 2.000 peak 8992) BrD = and resid 102 and r BrD = and resid 26 and r 1.700 1.700 peak 9	50 - 60 2.000 2.000		1.300 esid 21	2.200 esid 21	2.000 meid 21	2.900 2.100 2.100 [9222] eegid "BrD " and resid 21 eegid "BrD " and resid 18	2.100	1.600 1.600 1.600 1.600	1.600 1.600 1814 50	2.400 mid 50	2.000 sid 50	3.600 1.600 BrD and resid 101	_bry - and resid lot and n 2.200	"BrD " and resid 96 and r 1.600 1.600 peak 9	BrD and resid 101 and n BrD and resid 101 and n 1.100 1.100 peak 9	BrD and resid 101 and "BrD" and resid 98 and	0.0	2.200 2.200 peak 1	1.600 1.600 BrD " and resid 26	1.600 1.600	1.300	### ### ### ### #### #################	(eegid "BrO " end resid 13 (eegid "BrO " end resid 13 2.00
	ASM (9002) (9491d 'B (9491d 'B	A£81 (9012) (eegid ((eegid 2.800	ASSI { 9062} ({ megid "B (megid "B	AS81 (9082) ((9691d °	3.000 ASSI (9092) ((emgid (3.800 ASSI (9182) (eegid '	2.900 ASSI { 9222} (eegid (2.900 ABSI (9242) ((eegid '	2.500 A8SI (9292) (segid ((segid	A651 (9102 (8691d '	ASSI (9312) (eegid (2.800 ASSI { 9322 segid ' segid '	2.500 ASSI { 9112 ((megid '	3.000 ASSI (9342) ((eegid *	1(megid 2.500 ASSI (9372)	((segid ((segid 2.300	Assi (9422 (eegid) (eegid)	ASSI (9432) (1 segid '	3.000 ASSI (9442) ((eegid	2.700 ABBI { \$712} ((segid =	(1 eegid = 2.500 ASSI [9762] ((eegid =	((megid 2.300	((eegid (2.400 ASSI (9702)	((eegid ((eegid 2, 800 Add (9002) ((eegid

3.769 ppm2

2.346

3.769 ppm2

3.703

3.769 ppm2

1.15

5.479 ppm2

5.445

2.685 ppm2

5.41

2.340 ppm2

4.296

2.686 ppm2

1.25

2.341 ppm

2.781 ppm2 2.585 ppm2 3.304

1.947 ppm2

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5.541 ppm2

4.904 ppm2

4.904 ppm2

4.756 ppm2 4.359 ppm2 1.55

4.360 ppm2

5.143

2.634 ppm2

5.163

2.501 ppm2

2.78

5.051 ppm2

5.046

2.586 ppm2

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4.858 ppm2

4.297

2.286 ppm2

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0.52255£+03 ppm1	0.74419E-02 ppm1	0.10562E+01 ppm1	0.14866E+03 ppm1	0.14118E+03 ppm1	0.34604E+03 ppm1	0.13575£+03 ppm1	0.116765+03 ppm1	0.76235£+02 ppm1	0.53477E+03 ppm1	0.59437E+03 ppm1			0.15710£+03 ppm1	0.11776E-03 ppm1	0.48585402 ppm1	0.47917E+02 ppm1	0.151168-03 post			0.125728.03 ppm1	0.94017E+02 ppm1	0.13261E+02 ppm1	0.10292E+03 ppm1	0.56479E+02 ppml	0.52899K+02 ppm1
0.11000E+01 volume	0.11000E+01 volume	0.114896E+81 volume	0.11000E+01 volume	0.11900E.01 volume	0.11000E+01 Volume	0.11000E+01 volume	0.11000E-01 volume	0.11000E+01 volume	.0.11000E+01 volume	0.11000E+01 volume			0.11000E+01 volume	0.11000E+01 volume	0.11000E+01 volume	6.11000E+01 volume	0.11000K.01 volume	į		0.1100d6:01 volume	0.11000E-01 volume	0.11090K+01 volume	.11000E-01 volume	.11000E+01 volume	0.11000f.01 volume
HO1 1)	HOZA)	HB1 >>	and name HA)) and name HB1)) peak 10802 weight 0	and name HA 1) and name HB2 1) mesk 10812 weight	and name HB1)) and name HA)) peak 10822 weight o	and name MA)) and name HB1 }) sat 10917 weight	and name HA)) and name HB2)} eak 10942 weight	and name HA 1) and name HD1)) weak 10952 weight	and name MO2)) and name MD1)) peak 11002 weight .0	and name HD1)) and name HA)) seek 11032 weight	and name HA)} and name HB1)} seak 11092 weight	and name HD1)) and name HB2))	MD1	a ight		and name HD2)) and name HG2N) peak 11182 weight 0	and name HO1 1) and name HD1 1) peak 11212 weight 0	HO2))	HG2))	MO1))	a ight	MG2V)	peak 11272 weight o		and name MB2)) and name MD1%) peak 11302 weight 0
1.300	2.300	ard and resid 9 ard and resid 9 1.600 1.600	2.000 2.000	rD * and resid 20 rD * and resid 20 2.100 2.100	rD * and resid 24 rD * and resid 24 1.600 1.600	rD * and res	and r. 2.200	and r	D * and resid 44 D * and resid 44 1.300 1.300	rD * and resid 44 rD * and resid 41 1.300 1.300	CD * and resid 11 CD * and resid 14 2.200 2.200	of and resid 11	r. occ 2.000 lrD and resid 11 lrD and resid 10	2.200 2.200	2.900 2.100	TO " and resid 53 TO " and resid 50 2.900 2.100	rD * and resid \$3 2.000 2.000	reald 53 reald 53	resid 53 resid 53	resid 53	2.400 resid 53	resid 50 1.200 resid 19	2.200	segid BrD and resid 63 3.300 2.700 2.200 g [[11302]	2.100
((segid ' 2.300 ASSI (10762)	1123	11.3		((segid BrD ((segid BrD 2.900	- 0 0 0 ~	0000	1.000	200	(segid "Br			ASSI {11112} ((segid 'Bi ((segid 'Bi	ASSI (11122) (aegid "E (aegid "E				(segid	-:::	A881 (11232) ((segid ((segid	ASSI {11242} ((asgld '(3.100 A891 (11252) ((esgid	{	ASE (11292)	1, 1,300 3,300 A881 (11302)), 400 1, 400
2.780			;	3.021	1.145	2.729	2.731	1.731	4.738	4.63	4.547	2.931	2.847	2.662		2.662	2.181	4.99	2.702	2.60	4.951	4.951	£.633	4.672	; ;
4.854 ppm2	:			2.585 ppm2	3.782 ppm2	4.801 ppm2	4.831 ppm2	2.570 ppm2	2.694 ppm2	2.664 ppm2	2.684 ppm2	4.509 ppm2	4.509 ppm2	3.523 ppm2	:	3.227 ppm2	\$.000 ppm2	2.141 ppm2	\$.000 ppm2	5.000 ppm2	2.536 ppm2	3.583 ppm2	2.536 ppm2	2.504 DOM2	
0.30668R+03 ppm1	000000000000000000000000000000000000000			0.472735+03 ppml	0.42729E+02 ppm1	0.46141E-01 ppm1	0.56402E+03 ppm1	0.48724E+03 ppm1	0.12901E-04 ppm1	0.44336E+03 ppm1	0.38447E+03 ppm1	0.361448.03 ppm1	0.39358K+03 ppm1	0.239618+03 ppm1		0.23485£+03 ppm1	0.251668+03 ppm1	0.30460g+03 ppm1	0.48749E+03 ppm1	0.87656E+03 ppm1	0.24800E+03 ppm1	0.24031E+03 ppm1		0.13620E+03 ppm1	
0.11000E+01 volume	- 10000 10 mm	<u> </u>		0.11000E+01 volume	0.11000E+01 volume	0.11000K+01 volumn	ol volume	0.11000E+01 volume	0.11000£.01 volume	0.11000K+01 volume	0.11000E+01 volume	0.11000E+01 volume	0.11000E+01 volume	0.11000E+01 volume		0.11000£+01 volume	0.11000E+01 volume	0.11000E+01 volume	0.11000E+01 volume	0.11000E+01 volume	0.11000E+01 volume	0.116068+01 volume	0.11000E+61 volume	0.11000E+01 volume	
and name HA)) and name HB1)) peak 10322 weight			HB2 13	peak 10152 weight and name HG2)) and name HD10)	0392	Me ight	peak 10422 weight and name HB2 }) and name HA }}	peak 10452 and name and name	peak 10462 weight and name HB1)} and name HA 1)	e19ht	peak 10492 weight	peak 10532 weight	HBZ))	and name HOI)) and name HEN) peak 10552 weight	103	4 19 pc 19 p	#19h	0642 weight	1 de 1	and name HB2)) peak 10662 weight	and name HB2) and name HA) peak 10672 weight	and name HB1)) and name HA)) peak 10682 weight	and name HB2 1) and name HA)) peak 10692 weight	and name HB1 }} and name HA }} peak 10702 weight	and name KA))
maid 87	esid 67	14 84 84 84 84 84 84 84 84 84 84 84 84 84	resid 87	1.300 resid 87	2.000 resid 48	1.400 meid 94	1.300 20 pies	1.300 e pi 92	1.000 1.000 rD * and resid 112 rD * and resid 109	1.400 1.400 rd resid 112 rd and resid 112	1.400	1.600	1.400	25 Dise 27 Dise 27 J. 700	esid 75	1.700 esid 66	1.700 seid 66	1. 600 2. 600	1.300 1.300	1.100	irD * and resid 80 irD * and resid 77	1.700	2.200	ceid 80 seid 80	P. P. P.
ASSI (10322) ({ megld "Bi ({ megld "Bi (megld "Bi		ASSI (10342) ((segid "BrD " and 1 ((segid "BrD " and 2, 100	A551 [10352] ((megid "BTD " and ((megid "BTD " and	2.100 1.300 AESI (10392) ((eegid "BrD " and i eegid "BrD " and i	3.500 3.100 ASSI (10402) ((segid "BrD " and (segid "BrD " and	2.400 1.400 ASSI (10422) ((megid "BrD " and I ((megid "BrD " and I	2.300 AGBI (10452) ((megid "Bi ((megid "Bi	2.300 1.300 A&81 (10462) ([megid "BrO " and r ([megid "BrO " and r	2.000 ASSI (10462) ((megid "Br ((megid "Br	2.400 ASSI {10492} ((eegid "Br	ASSI (10512) ((segid "BrD " and r	2.500 2.500 ASSI [10542] ((segid 'Br	({ segid "Br 2.400 ASSI (10552)	(eegid 'BrD ' and a eegid 'BrD ' and a 2.600 1.700	ASSI [10562] ((megid "BrD " and r (megid "BrD " and r	2.600 1.700 ASSI (10632) ((eegid "BrD " and r ((eegid "BrD " and r	2.600 ASSI (10642) ((segid "BI	2.500 1.600 ASSI (10652) ((eegid "BrD " and r	ASSI (10642) ((aegid "Br	((eegid *B: 2.100 ASSI (10672)	((segid 'BIO and 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	(segid BrD * and r ((segid BrD * and r 2.600 1.700	ASSI (10692) ((segid 'Br ((segid 'Br	ASSI (10702) ((megid "Bi ((megid "Bi 2.900	Assi (10752) ((eegid 'B

4.801 ppm2

1.7

4.608 ppm2

2.351

4.403 ppm2

2.857

4.901 ppm2

2.33

4.655 ppe2

2.5

4.953 ppm2

2.931

4.901 ppm2

1.901

4.655 ppm2

2.337

4.803 ppm2

4.337

2.645 ppm2

5. SE

4.312 ppm2

2.471

4.951 ppm2

3.300

4.457 ppm2

3.35

4.457 ppm2

5.446

4.263 ppm2

. 93

4.015 ppm2

4.209

2.784 ppm2

4.210

2.490 ppm2

4.011

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4.011

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0.33

2.784 ppm2

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1.688

1.988 ppm2

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0.13883E+03 ppm1	0.123068+03 ppm1	0.11534E+03 ppm1	0.97643E+02 ppm1	0.132438+03 ppm1	0.13995E+01	0.141468.01	40.24		C. Ledyskyoz ppm.	0.52760E+03 ppm1	0.19334E+03 ppm1	0.59031E+02 ppm1		0.90578£•02 pm1	0.130578+03 ppm1	0.30078E+03 ppm1		0.10826E+03 ppm1	0.42931E+03 ppm1	0.811178.03 ppm1		and bourses	0.42022K+03 ppm1	0.403198+02 ppm1	0.38368E+03 pgm1	0.51224E+03 ppm1	0.51311K+03 ppm1
0.11000E+01 volume 0.13883E+03	0.11000\$+01 volume	0.110008+01 volume	0.11000E+01 volume	0.11000E+01 volume	0.11000E+01 volume	0.11000E-01 volume				0.11000E+01 volume	0.11000E.01 volume	0.11000E+01 volume		0.110005+01 volume	0.11000E+61 volume	0.11000E+01 volume		0.110006.01 volume	0.11000E+01 volume	0.11000E+01 volume	200011 0		0.110605.01 volume	0.11000E+01 volume	0.11000E+01 volume	0.11000£+01 volume	0.11600E+01 volume
and name peak 12032	Pack 12042	and name and name pack 13062	and name and name pask 12072	and name HD1)) and name HG2)) peak 12062 weight	and name HD2)) and name HG2)) peak 12092 weight	and name MB1)} and name MG2)} pask 12103 weight	and name and name	and name	and bas	peak 12222	and name yeak 12342	and name MA)) and name MB2)) peak 12252 weight	and name HA 1)	end nem	and name peak 12272	and name HB1)) and name HA)) peak 13312 weight	and name	Post 12322	and name KA)) posk 12332 weight	and name MB2)) and name MA)) peak 12342 weight	resid 102 and name HD20) resid 102 and name HG 1) 1.000 mak 12382 seinhr	resid 102 and name KD2t)	setd 102 and name MD24)	peak 12422 weight	and hame peak 12432	and name MD10) and name MB2)) peak 12442 weight	and name HD10) and name HB1)) peak 12452 weight
*BrD * and resid 33 2.100 2.100	2.900 2.100 2.100 (12062)	segid 'BrD' and resid 33 3.000 2.200 2.200	BrD - and resid 33 2.400 - 2.400	2.300 2.300	rD * and resid 33 rO * and resid 33 2.100 2.100	2.10	2.60.2	[[12162] [eegid "BrD " and resid 15 [eegid "BrD " and resid 16 4.100 4.100 1 400	es pre	1. 100 14 59	1.800 1.800	2.200	segid 'BrD ' and reald 59 segid 'BrD ' and reald 62	4.400	2.100	1.600	19 pt e	2.200		2 P 1 . 1	1000 T	(12402) megid "BrD " and resid 102 megid "BrD " and resid 102			1.400 1.400	1 1 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1.300
((eegid '8 2.900 A861 (12042)	((aegid '8 2.900 A581 (12062)	((segid ") 3.000 Asst (12072)	((eegid 'B: 3.100 ASBI (12062)	((aegid "g ((aegid "g 2.900 ASSI (12092)	((segid '8) ((segid '8)	(aegid *	ASSI [1213] ([megid "Be ([megid "Bi) tou	ASSI [12162] ([aegid "E ([aegid "E 4.100	ASSI (12222) ((megid "B (megid "B	2.300 ASSI (12342) ((segid "6	2.700 A881 (12252)	8 piges)) 8 piges)) 1,300	(ASSI (12272) ((megid "B		((eegid "B ((eegid "B	ASSI (12322) ((megid "8 (megid "8	3.000 A681 (12332)	((megid = 8 2.400 ASSI (12342)	(segid "B	Assi (12392) (eegid "B ((eegid "B 2.000	ASSI (12402) (megid "B (megid "B	ASSI (12422) (segid *8 (segid *8	3.500 ASSI (13432) (segid *8	([segid "B 2.400 ASSI (12442)	(mg1d mg (mg1d mg 2.300 ASSI (12452)	(segid 'BrD * and re ((segid 'BrD * and re 2.300 1.300
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2.43	97.				0.766	4.667	4.667	2.291	1.646	2.323			116.3	4.406		2.978	2.788	5.643		3	4.559	4.559	5.378	.0.319	991.0		1.083
4.805 ppm2	2.685 ppm2	2.420 mm3		7.340 ppm2	2.340 ppm2	2.636 ppm2	2.190 ppm2	4.972 ppm2	2.291 ppm2	3.177 ppm2		rudd 679.7	3.17 ppm2	2.779 ppm2		5.347 ppm2	5.347 ppm2	4.559 ppm2		4.410 ppm2	2.730 ppm2	2.978 ppm2	2.725 ppm2	4.361 ppm2	4.341 poss		4.360 ppm2
0.408738+03 ppm1	0.64841E+03 ppm1			tude to server of	0.122618+03 ppm1	0.482018+03 ppm1	0.27263K+03 ppm1	0.40526K+03 ppm1	0.262438+03 ppm3	0.19040E+03 ppm1			0.81736E+62 ppm1	0.11953R+03 ppm1		radd coestress.	0.32384E+02 ppm1	0.19122E+03 ppm1		0.16587E+03 ppm1	0.31825£+02 ppm1	0.50256&+02 ppml	0.17033E+03 ppm1	0.10731E+03 ppm1	0.20069E+03 pcm1		0.186698+03 ppm1
0.11000K+01 volume (0.11000G.01 volume (volume	1		0.11000E+01 volume 0	0.11000E-01 volume c	0.11000E+01 volume c	0.11000E+81 volume o	0.11000K+01 volume C	0.11000E+01 volume 0	0.11000001.0		0.11000E+01 volume 0	0.110008+01 volume q			0.11000E+01 volume 0	0.11000E+01 volume 0		0.11000K+01 Volume 0	0.110008+01 volume 0	0.11000£+01 volume 0	0.11000E+01 volume 0	0.11000E+01 volume 0	0.11000E+01 volume 0	•	0.11050K+01 volume 0
		(101) (101)	1111	HB1))	weight HBi)) HA))	We 1ght HO1))	MA 19ht		e ight	and name RG1)) peak 11712 weight 0	and name HD2)) and name HG2)) Deak 13732 weight o		eight to 1)		and name NA 1) and name NB1))	and name HA))	11812 Weight	and name HD1 }) and name HA }) tak 11852 weight	and name HD2))	and name HB2)	e ight	ak 11922 weight	and name HA)) ak 11942 weight	and name HG2)) ak 11952 weight	and name HA)) and name HB2)) peak 11962 weight 0	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	welghe HG1 1)
(11392)	D - and resid 97 D - and resid 94 1.200 1.200 p	D * and resid 97 D * and resid 97 3.200 1.900 p	seid 66	98 pt 88	resid 64	resid 64	1.70	1.400	1.700 1.700	1. 500	mid 62 mid 62 2.300	seid 62	2.400	2.300	16 bis	D and resid 91	1.700 1.400 1.800 po [1 [11852]	D - and resid 91 1.800 1.800 p	te pies	D and resid 91	1.800	2.900 2.100 p	(megid "BrO . and resid 91 2.000 2.000 2.000 pm If [11952]	2.200 2.200 p	1.800	tt bies	
(11392) (segid Br: (segid Br: 2.400	(megad "Bri (megad "Bri 2.200		[{11472} { eegid "BrD " and z { eegid "BrD " and z 2.400 1.400	[(11462) segid "BrD = and r segid "BrD = and r	LBSI (11612) ((Aegid BrD * and ((aegid BrD * and	2.300 ii (11622) (megid "Brf (megid "Brf	2.600 1.700 1 (11692) (megid 'hib ' and t	2.400 1.400 [[11702] [megid "BrD " and r	2.600 1.700 1 (11712) 6 megid "BrD " and r	(megid "Brf 2.700 [(11712)	(segid 'BrD 1.200	[(11742) segid 'StD ' and r segid 'BzD ' and r	3.100 [{11782} (segid *BrD	(segid "BrD " and r 3.000 2.200 I (11802)		1 (11612) (eegid 'BrD (eegid 'BrD	1 (11852)	2.700	(11862) (megid 'Bri (megid 'Bri	[(11913) (aegid 'BrD " and r (aegid 'BrD " and r	1.700 3.400 1 (11922) (segid "BrD * and	1,400 1 (11942) (megid '8rb	(eegid "Brr 2.800 [(11952) [eegid "BrD	3.000 1.000	(segid 'BrD ' and r (segid 'BrD ' and r 2.700 1.800	Assi (11972) ((megid "BrD " and r ((megid "BrD " and r	[{12033} [segid 'BrD ' and
A881	===	788 2	7881 7	7881 1131	7881	. Ves	YB81	1884	1884) (B\$4		7881 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Yes) 1884		ABB	ASSI	!	, , , , , , , , , , , , , , , , , , ,	7881	1381	1984	1884)	į==	A88	į

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-0.324 ppm2

0.858 ppm2

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9.6

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-0.319 -0.319 -0.316

2.780 ppm2

2.189 ppm2 1.051 ppm2 46.0

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3.137 ppm2

1.176

2.487 ppm2

2.417

4.903 ppm2

2.657

4.903 ppm2

1.670

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4.63

2.626 ppm2

4.451

2.626 ppm2

1.45

2.679 ppm2

4.62

2.679 ppm2

2.159 2.020

1.304 ppm2

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egid BrD 200 2.	(eegid BrD (2.300 1. ASSI (13372)	(13382)	2.600 1. (13402)	2.600 1. (11422)	914 BrD 914 BrD 700 3.	2.700 3.70 (11442)	2.900 3. (13462)	2.800 2.610 (13492)	4914 BrD -	(eegid "BrD " (eegid "BrD ").100 2.4	megid BrD = megid BrD = 3.400 2.4 (13542)	segid 'BrD ' segid 'BrD ' 3.200 2.(((eegid 'BrD -) 3.300 2.3	(segid *BrD * ((segid *BrD * 2.800 2.0	((segid 'BrD ' segid 'BrD ' 3.700 3.4	((megid BrD = 1.6 megid BrD = 3.6 megid BrD =	aegid *BrD * aegid *BrD * 2.600 1.7 (13742)	eegid BrD - 2.300 1.3	aegid BrD 3.700 3.4 (13912)	(segid BrD - 2.0 2.0 2.0 2.0 (13932)	((megid "BrD " 3.400 2.9 ASSI (13942)	((aegid BrD * 3.300 2.7 A691 (14002)	ora. pie
) 1881) 188Y	1884	7.5 2.6 2.6 1.0 1.0 1.0 1.0 1.0 1.0 1.0 1.0 1.0 1.0		ABSI C	VBBV	i i i	A881	V881	- 188V	YESI (2 189V	A881 C.C.	A581	7 188 V88		ASS! C.C.	73 13 13 13 13 13 13 13 13 13 13 13 13 13	(eegid 'B 3.700 ASSI (13912)	(segid B) 2.600 ASE (13932)	AS81 (1	A891	Ξ,
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0.239718+03	0.29352K+03	0.21211E.03	0.886346+03		0.354148+03	0.140\$7E+03	0.66311E+02	1868.03	0.509768+02	1338.03			3				U. 59764K+02		0.483038+03		0.168928+03	0.879448+02	
								r 0.17186E												378385	0.16	9.879	
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0.11060E+01 volume	0.11600K+01	0.11000E+01	0.110006+01	0.110005.01	0.110006+01	0.110006+01	0.11000E+01	0.11000E+01	0.11000E+01	0.11000E+01	0.110000.01	10,0001						0.11000E+01	0.110006+01	0.11000E+01 volume	0.110006+01	0.11000\$+01	
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A and name HD11) 1 and name KA)) 2 peak 12462 weight	and name and name peak 12472	and name and name peak 12602	and name and name peak 12622	and name and name i	and name and name peak 12682	and name and name peak 12772	and name and name peak 12802	and name and name peak 12902	and name and name peak 12912	and name and name peak 12922	and name and name beat 12932	and name) 2 and name) Deak 12942	and name	and name and name	and name and name	and name	and name and name peak 13162	and name and name peak 13172	and hame and name peak 13182	and name and name peak 13212	and name and name peak 13222	and name and name peak 13252	and name
226	11d 14			1. 800 pe	3.28	2:0	2 2 2	7 7 8	2 8 8	888	# # 5	102	2.400 pre	2.300 De	3 7 8	10 20	1d 88 2.100 pe	1.00 Pe	1.300 Pe	1.900 Pea	2 2 2	Δ.	
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66.	66	6 6 8 4 8	9	6.6	6.6	id 'BrD and id 'BrD and oo 2.100	14 BrD and 14 BrD and 10 2.700	2.000	2.300	370 * and 3.900	And 1.	, 100 m	4 4 6	2 4 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	0 * and	20.0	2 0 0	66	1. 300	200 a to	2.000 tand	2.400	
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2.323	2.13		į		9							1.211	7. 883				2.634	2.905	1.544	4.410	4.00	3.46	£.30
4.104 ppm2	1.054 ppm2	2.441 ppm2	1.795 ppm2	1.842 ppm2		. 003 Canada	500		2. 426 mm2			1. 14 ppm3	t. 140 pp.2	2. 974 ponz		2.78	4. 903 ppm2		4.756 ppm2	1.596 ppm2	1.787 ppm2	4.804 ppm2	1.781 ppm2
0.75137E+02 ppm1	0.50793K+03 ppm1	0.18691E+02 ppm1	0.200968+03 ppm1	0.262458+03 ppm1	0.297808+02 ppm1	0.19090E+01 ppm1	0.14250E+03 pgm1	.175748-03 pps1	1.345928+02 ppm1			Tedd Towns		. 16084Red Pomi			0.25810E+03 ppm1	.59564E+03 ppm1	0.30496E+02 ppm1	0.17496E+03 ppm1	55145E+02 ppm1	.65568K+02 ppm1	160438.03 ppm1
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esid 56 and name MG) 2.300 peak 13262 weight	resid 18 and name KD1%) resid 18 and name KB1)) 1.300 peak 13362 weight	esid 14 and name MB1) esid 18 and name MD10 1.500 peak 13372 weight	resid 25 and name NG19) resid 22 and name NA 3) 3.700 peak 13382 weight	resid 102 and name NB2)) resid 99 and name NA)) 1.700 peak 13402 weight	resid 21 and name HB)) resid 18 and name HD2%) 1.800 peak 13422 weight	resid 57 and name NB2)) resid 60 and name NB2)) 1.800 peak 11432 weight (resid 58 and name MG25; resid 62 and name MG2 }) 2.000 peak 13462 weight C	resid 61 and name HB1)) resid 50 and name HG2t) 1.900 peak 11492 weight G	resid 59 and name HEt) resid 59 and name HA)) 2.400 peak 13512 weight o	resid 59 and name MRk) resid 56 and name MD2k) 3.100 peak 13522 weight o	and name HA)) and name HB2)) Peak 13542 watch:	and hame NB2 }) and name NA)) Peek 13552 weight	and name and name peak 13652	resid 32 and name HA }) resid 31 and name HBb } 1.800 pask 13662 weight o	_	resid 59 and name HA)) resid 62 and name HD2)) 1.700 peak 13722 weight 0	resid 63 and name HG)) resid 63 and name HB1)) 1.300 peak 13742 weight o	resid 70 and name HB1)) resid 69 and name HG1%) 1.600 peak 13902 weight 0	and name and name ak 13912	and name HG12)) and name HA)) seak 13932 weight		and by and name MB1)) and 53 and name MD1)) 2.000 peak 14002 weight 0.
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4.010	3. 606	3.697	4.683	2.434	1.750	4.460	4.942	4.984	1.633	4.425	2.274	2.587	1.710	2.340	7.421	6.69	6.683	\$.578	5.575	7.315	5.762	1.211
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2.741 ppm2	4.409 ppm2		2.680 ppm2	4.830 ppm2	4.901 ppm2	2.540 ppm2	2.145 ppm2	1.303 ppm2	1.305 ppm2	1.303 ppm2	0.911 ppm2	8.447 ppm2	\$66 ppm2		4.163 ppm2	4.164 ppm2	.078 ppm2	.372 ppm2	3.570 ppm2	2.639 ppm2	.705 ppm2	3.376 ppm2
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0.109298+03	0.111238+03	0.673148+02	0.381868.03		0.374718+03	0.21551E+03	0.587228+02	0.517686+02	0.507476+03	0.22765E+03	0.946238+02	74 B • 00	536.02	04 - 02	0.19889E+03	0.362188+02	758+03	0.985306+02	2	0.17734E+02	028+03	0,56146E-02
0.1093	•.111.	0.673	0.381	0.686368.02	0.374	0.215	0.547	0.517	0.507	0.227	0.9	0.4837484	0.740538+	0.27804E	0.198	0.362	0.286758+	0.985	0.74212E+	0.177	0.164028	9.5
o) tan	volume	volume	volume	volume	volume	volume	volume	voluse	volume	volume	volume	volume	valume	volume	vol une	volume	volume	volume	volume	volume	voluse	Volume
											10.30											
0.11000\$+61 volume	0.110005.01	0.11000E+01	0.11000E+01	0.11000E+01	0.11600B+01	0.11000E+01	0.116005+01	0.119006+91	0.11000E+01	0.11000E+01	0.11000\$+01	0.114008+01	0.110006+01	O.11000K+01	0.11000E+01	0.110005+61	0.11000B+¢1	0.11000E+01	0.11000E+01	0.11000E+01	0.110008+01	0.11000E.01
KB1)) KD2))				HA))	HAZV)	HB2 1) HD1 1) weight	KB2)) KA))	KD2V) KA))	HD2V) HO2V)	HD2V) HA)) weight	HB2)) HO)) weight	HG2	<u>F</u>		HA 11 HB1 1 veight	HA 1) HE 1 weight		HB2 1) HD2 1) weight	HB1)) HD2))	HB1)) HEL) weight	KDA)	HEN) HEN) Weight HB1))
Ame KB	3 E S	2 H Z	AMP HA	5 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	1 1 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	Ame HB Ame HD SS2 wo	57.2 KB	5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	전 등 등 등 등 등 등 등 등 등 등 등 등 등 등 등 등 등 등 등	6 2 2 2 3 3 4 3 4 3 4 3 4 3 4 3 4 3 4 3 4	# # C C S	583	Ame HB2 Ame HB4 812 veig	22 H H	342	262 E	A Series	0 6 2 H	A HE HE	Dame HS Dame HS	3 2 3 3	
and name and name peak 14012	and name and name peak 14072	and name and name peak 14082	and name and name peak 14092	and name and name peak 14182	and name and name pask 14252	and name and name peak 14552	resid 14 and name F resid 11 and name F 2.200 peak 14572 v	eld 102 and name held 31 and name 2.100 peak 14592	and name and name peak 14612	12 and name and name peak 14622	and name and name peak 14662	and name and name peak 14772	and name and name peak 14812	and name and name peak 14822	and name and name peak 14942	and name and name peak 14962	and name and name peak 14992	and name and name peak 15062	and name and name peak 15072	and name and name peak 15122	and name and name peak 15292	and name and name peak 15322
BrD and resid 53 BrD and resid 53 2.200 2.200 p	resid 79 resid 82 2,200 g	reeld 79 reeld 62 2.200 F	resid 75 resid 76 1.400 g	resid 94 resid 97 2.300 p	resid 113 resid 17 1.900 p	resid 11 resid 11 1.800 p	# 1 8 P 2 1	reeld 102 reeld 31 2.100 p	resid 102 resid 25 1.300 p	resid 102 resid 25 1.800 p	resid 18 2.400	resid 16 resid 37 0.000 p	resid 42 resid 43	resid 35 1.700	resid 46 resid 88	resid 46 resid 46 1.900	1.600 1	reeld 28 reeld 28 2.400	resid 28 resid 28 2.300	822	5 2 8	14 47 2.100 14 47
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		e e ·	200	6.0	20		gid BrD and gid BrD and 300 2,700	C. C.	2 2	14 'BrD and 14 'BrD' and 1000		200	4812) gid 'BrD " and gid 'BrD " and 200 2.600	314 'BrD and 314 'BrD and 314 'BrD and 800 3.600	[14942] segid BrD * and r segid BrD * and r 2.700 1.800		20	55	megid 'BrO " and megid 'BrO " and 3.200 3.600	6. 2	20	megid 'BrD aegid 'BrD 1.400 2 (18112)
(14012) eegid 'BrD eegid 'BrD 1.000 2	[14072] segid "BrD " and segid "BrD " and 1,000 2,200	[14082] segid "BrD and segid "BrD and 3.300 2.700	segid BrD and segid BrD and 2.400 1.400	[14182] eegid "BrD " and eegid "BrD " and 3.200 2.600	######################################	segid BrD and a	2.300 3.300	segid "BrD" and in and	segid BrD and r segid BrD and r 2,300 1,300	2. 700	[14642] eegid BrD and 1 eegid BrD and 3, 100 2, 400	[44772] [44914 BrD * and r [44914 BrD * and r 5.500 5.500	(1481 aegid aegid 1.200			[14962] segid 'BrD ' and r segid 'BrD ' and r 3.600 3.200	(segid 'BrD ' and r. segid 'BrD ' and r. 3.700 3.400	3.100	3.200	eegid 'BrD ' and r eegid 'BrD ' and r 4.100 4.100	segid BrD and segid BrD and and segid BrD and segid se	
7		¥ = = ;			1 - 1	==		i i	i i	i	# = = :	===	7881 	# = = = = = = = = = = = = = = = = = = =	1 - 1	,) - IS84)	~ ~ 188 4	, , , , , , , , , , , , , , , , , , ,	=	- W

7.271	7.952		1.833	7.535	7.069	7.069	7.063	7.259	0.40	7.901	1.601	2.494	4.932	4.932		7.707	55.5	1.91	7.70\$	5.542	\$.36	*:	-0.162
3.816 ppm2	3.962 ppm	3.576 ppm2	2.985 ppm2	1.571 ppm2	3.573 ppm2	3.672 ppm3	4.755 ppm2	4.755 ppm2	4.607 ppm2	4.410 ppm2	4.410 ppm2	5. 592 ppm2	3.721 ppm2	3.668 ppm2	3.720 ppm2	4.903 ppm2	4.804 ppm2	4.804 ppm2	3.125 ppm2	0.760 ppm2	0.755 ppm2	0. 859 ppm2	2.190 ppm2
0.74345E-03 ppm1	0.274986+03 ppm1	0.14689E.03 ppm1	0.17941E-02 ppm1	0.16094K+03 ppml	0.116\$\$\$*03 ppm1	0.15106K-03 ppm1	0.68425E+02 ppm1	0.82\$72£.03 ppm1	0.83712E-01 ppm1	0.21131E+03 pps1	0.169048-03 pgm1	0.97231E+00 ppm1	0.25356E+03 ppm1	0.43854E+03 ppm1	0.672428+03 ppm1	0.69463E+03 ppm1	D.16843E+03 ppm1	0.94615B+02 ppm1	0.12277E+03 ppm1	0.3115#E+03 ppm1	0.23078K+03 ppm1	0.93743E+02 ppm1	0.10412E+03 ppm1
11000E-01 volume	11000K+01 volume	11000E+01 volume	0.11000K+01 volume	0.11000K.01 volume	0.11000E-01 volume	0.11000E-01 volume	0.11000E+01 volume	0,11000E-01 volume	11000E-01 volume	0.11000E+01 volume	0.110008.01 volume	0.11000E.01 volume	0.11000K+01 volume	0.11000E+01 volume	0.11000E+D1 volume	0.11000£+01 volume	0.11000E+01 volume	0.110005.01 volume	0.11000E+01 volume	0.11000E+01 volume	0.11000E-01 volume	0.11000E+01 volume	11000E-01 volume
hamm HEt) 5312 weight O.	name KB2)) name HE3)) 5152 weight 0.	name HB1)) name HB4) 1432 weight 0.	MANNE HEL) MANNE HEL) MANNE WEIGHT	KB1)) KE1)	name MB2 }} name ME4 } 15602 weight 0.	tame HB1)) tame HE0) 1612 weight	HA 1) HEA 1	HDV)	name HA 1) name HD24) :5792 velght 0.	HEN))	HE 1)	HA 1) HA2 1)	HB1 1) HA 1)	HB2))	HB2 13	HA 11	HA 1) HG12))	and name HA)) and name HG11)) ak 17302 weight 0.	KB2 1) KDA 1	HO24) HA 11	HG2V) HA))	I name HG1)) I name HA)) 17727 weight 0.	name MD3 }} name HB3 }} 7812 weight 0.
resid 47 and name 2.300 peak 15332	resid 32 and name resid 32 and name 1.700 peak 15352	resid 74 and resid 74 and 2.100 peak 1	resid 74 and resid 74 and 1.900 peak 1	resid 74 and name resid 74 and name 2.000 peak 15492	resid 82 and resid 82 and 2.200 peak	resid 62 and 2.000 peak 1	resid 82 and name resid 82 and name 2.300 peak 15732	resid 82 and name resid 82 and name 1.100 peak 15742	resid 15 and resid 18 and 0.900 peak 1	resid 107 and name resid 107 and name 1.800 peak 16522	resid 96 and name resid 96 and name 2.000 peak 16532	resid 52 and name resid 53 and name 0.000 peak 16692	resid 105 and name resid 105 and name 1.700 peak 16822	2.5		resid 105 and resid 105 and 1.200 peak	resid 116 and name resid 116 and name 2.000 peak 17292	resid 116 and resid 116 and 2.400 peak 1	resid 34 and name resid 34 and name 2.100 peak 17412	resid 81 resid 34	resid 81 and name resid 55 and name 1.700 peak 17652	resid 33 and resid 33 and 2.400 peak 1	resid 33 and resid 33 and 2.200 peak 1
egid "BrD and 1.200 2.600	segid BrD and 1	segid Bro and	egid BrD and egid BrD and 1.600 3.200	segid BrD and	segid BrD and segid BrD and 3,000 3.200	segid BrD and	megid BrD and megid BrD and 3.200 2.600	segid 'BrD and segid 'BrD and 2.100	megid 'BrD and megid 'BrD and 4.600 4.600	segid BrD and 2,700 1,600	arD and arD and 2.000	segid BrD and	segid BrD and segid BrD and 2.600 1.700	(17182) megid 'BrD ' and megid 'BrD ' and 2.400 1.400	5 - 5 - 5 - 5 - 5 - 5 - 5 - 5 - 5 - 5 -	17142} segid "BrD " and segid "BrD " and 7.200 1.200	BrD and BrD and 2.000	17302) segid BrD and segid BrD and	170 • and 170 • and 2.100	70 and 7. 1. 600	17662) eegid 'BrD ' and eegid 'BrD ' and 2.600 1.700	egid BrD and segid BrD and 1.100 2.400	14.000 2.200
- 104							= -					==		7881	A881	Yest	7881	788				==	==

	2,600 1.700 1.	(segid 'BFD ' and reald 43 (segid 'BFD ' and reald 8s 2.500 2.100 2.100 ASI (1912)	megid 'BrD ' and megid 'BrD ' and 4.900 4.900 [19142]	segid "BrD and segid "BrD and 3.400 2.900 (19162)	eegid 'BrD ' and eegid 'BrD ' and 2.600 1.700 [19852]	eegid 'BrD ' and eegid 'BrD ' and 2.700 1.800 {20062}	aegid BrD and 2.400 1.400 (20212)	segid BrD and re segid BrD and re 1.100 2.400 (20142)	megid BrD and segid BrD and 1.300 2.700 [20372]	eegid BrD and aegid BrD and 1.900 1.800 {20422}	## BrD and re ## BrD and re 3.200 2.600 {20432}	3.400 BrD 3.400 [20462]	(eegid "BrD " and resid 53 (eegid "BrD " and resid 46 3.400 3.200 3.200 A.500 pm	((eegid "BrD " and resid 5) (eegid "BrD " and resid 47 2.500 1.600 po ASE (20482)	(degid BBD and resid 53 (eegid BBD and resid 47 2.60 1.700 1.700 ps AGSI (2042)	((megid "BrD " and reaid 53 eegid "BrD " and resid 47 2.400 1.400 pt 1.400		eegid 'BrD ' and eegid 'BrD ' and 5.500 5.500 [20602]	eegid "BrD" and 2.500 1.600 [20612]	(segid "BID" and resid 61 (megid "Bro and megid Bro and 1.400 0.500 [20772]		eegid BFD and resid \$6	(segid "BTD " and reald 63
	69. 9.					7.79	91.	2.792	3.26.2	91.1			r. 90 91	6.688	7.267	7,962		1.901				<u> </u>		1.140
	2.262 pom2	2.190 mm2		2.190 ppg		2.191 ppm2			3,522 poet2	3,226 ppm2			zedd ser r	2.783 ppm2	2.743 ppm2	2.777 ppm2	2.781 ppe2	radd ye.	224 mag					2.634 ppm2
	0.99908R+02 ppm1	0.24295E+02 DDM1					0.210098+02 ppm1	8	60		0.17236K+02 ppm1						5			9				0.246356.03 ppm1
	0.11000E+01 volume 0			vol ume	volume		0.11000E+01 volume G.	0.110808+01 volume 0.		0.11000E+01 volume 0.	0.11000E+G1 volume D.								01 volume 0				•	0.5
	and name HD1) and name HB2) peak 17622 weight	and name and name peak 17832	and name and name peak 17842	and hame and hame peak 17862	and name and name peak 17872	and name and name peak 17882	and name HB1]) and name HD2) peak 17912 weight	and name MB1)) and name MD1 }) peak 17942 weight	and name HG1)} and name HG2v) mak 18062 weight	resid 75 and name MG2)) Feeid 110 and name HD1%) 2.100 pesk 18062 weight	02 J) 02N) •19ht	and name HS1)) and name HA)) peak 18162 weight	and name KB1)) and name KB1)) and name KEV)	and name HSt)	and name HA 1) and name HDt)	and name HSt) and name HSt) and habe HG1))	and name HSt) and name HA)) peak 18292 weight	and name HG2)) and name HD4) peak 18452 weight	and name and name peak 18462	and name HEN) and name HA)) peak 18512 weight o	and name HEL) and name HD21) wak 18752 weight	and name HE%) D and name HGZ%) peak 18792 weight o	and name HEt) D and name HD10)	and name (A))
	BrD * and resid 33 2.200 2.200	ord " and resid 33 300 and resid 33 3.600 1.600	110 * and resid 33 110 * and resid 33 3.600 1.700	(17862) segid BrD and resid 33 segid BrD and resid 32 3.300 2.700 2.200	0.000	117862] e=gid "BrD" and reaid 33 s=gid "BrD" and reaid 32 \$.500 • 5.500 0.000	te bi 33	resid 33 2.200		eegid 'BrD' and resid 75 eegid 'BrD' and resid 110 3.600 2.900 2.100	rD * and resid 75 rD * and resid 110 4.100 1.400 pe	10 53 10 53 0.000	1,700	18 td 47	2. 40 53	meid 35 1.300	atd 35	meid 75 meid 74 2.100	* and resid 74 * and resid 74 7.400 2.400	eeld 75 eald 75 2.100	resid 75 resid 18 1.700	1.800		4 reeld 75
100001 (1000)	((megid ') () () () () () () () () ()	006.c	B. pi6ee))	((megid "B ((megid "B ((megid "B	(megid "B (megid "B (megid "B	(megid "B (megid "B (megid "B 5.500		- 4 6 7 -		(megid 'B (megid 'B).400		(aegid '8 (aegid '8))	ASSI (16172) ((eegid "Bi (eegid "Bi 2.600	ASSI (18182) ((eegid 'B; (eegid 'B; 2.500	A651 [16192] {{ megid "BrD" and a { megid "BrD" and a 3.100 2.400	ASSI (18222) (segid "B: ((segid "B: 2.300	A881 [18292] (megid "BrD " and ((megid "BrD " and 2.700 1.600	ASSI {18452} {(segid "BrD " and r (segid "BrD " and a 1.400 2.900	ASSI (10462) ((eegid "BrD (segid "BrD).100	(segid 'Bi	(segid 'SrD' and (segid 'SrD' and)			A881 (19032)

,		7. 416		7.609	6.619		5.753	2.157		1.71	3.812				•							757	4.452	. 10	5.544	5.542	4.476
* ***	ļ	1.700 ppm2		1.697 ppm2	1.657 ppm2		1.697 ppm2	4.263 ppm2		4.411 ppm2	1.747 ppm2			20.5		3.784	3.786	2.4	7	2.784 pom2	2.784 pom2	2.431 ppm2	2.980 ppm2	1.656 ppm2	4.702 ppm2	1.648 ppm2	3.177 ppm2
0.28302E+03 ncm1		0.13602E+03 ppm1		radd measses	0.53713E+02 ppm1		d.zesttett.oz ppm;	0.19930E+03 ppm1		0.38344E-03 ppm1	0.91919K+02 ppm1	0.66608E+02 prest	0.22677E+02 pom1	0.75265R+02 ppm1	0.50650E+02 ppm1	0.3\$265K+02 ppm1	0.29199E-03 ppm1	0.271228+03 pps1	0.38647E+03 ppm1	0.162138-03 ppm1	0.50337E-01 ppm1	0.31153E+03 ppm1	0.36307E+03 ppm1	0.11465E+05 ppm1	0.51113E+02 ppm1	.15234E+03 ppm1	94082E+02 ppm1
0.11000E-01 volume		0.11000E+01 volume	. 11000F.01		0.11000E+01 volume		author to tack	0.11000E+01 volume		0.110005.01 volume	0.11000E+01 volume	0.11000£.01 valume	0.11000E+01 volume	0.11000K+01 volume	0.11000E+01 volume		0.11000£+01 volume	0.11000E+01 volume (0.11000E+01 volume (0.11000E-01 volume o	0.11000E+01 volume 0	008+01 valume o	0.11000E+D1 volume 0	00E+01 volume 0	00E+01 volume 0
we ight	1	1461 M	KD1 -	101	we 1ght	KBA)	(1 41 8	#0))	101101	1619h	a ight	KD1))	HA))	HD2)) HA))	HD1)) HG2()	HO1)) HEN)	HG1)) HEN)	HG2)) HE%) weight	HG2)} KD1 }	HO1 13	103 11 14 11 11	HG2 11 HA 11 weight	HG1 11 HA 11	HB))	16 19 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	MO24 HA weight 0.110	HD1
1.700 peak 19032	resid 43 and name	2.100 pask 191	resid 43 and name resid 88 and name 0.600 peak 19132	resid 43 and name	2.100 peak 19142	resid 43 and name resid 46 and name 1.700 peak 19162	resid 102 and nas	reeld 102 and ness 1.800 peak 19852	resid 110 and name resid 110 and name	of and peak 2001	2.400 peak 20232	resid 53 and name resid 53 and name 2.200 peak 20342	resid 53 and name resid 47 and name 1.600 peak 20372	resid 53 and name resid 53 and name 2.300 peak 20422	resid 53 and name resid 50 and name 2.100 peak 20432	resid 52 and name resid 46 and name 1.900 peak 20462	resid 53 and hame resid 47 and name 1.600 peak 20472	resid 53 and name resid 47 and name 1.700 peak 20482	resid 53 and name resid 47 and name 1.400 peak 20492	resid 53 and name resid 47 and name 2.000 peak 20502	resid 53 and name resid 52 and name 0.000 peak 20522	resid 61 and name resid 50 and name 1.600 peak 20602	resid 61 and name resid 58 and name 1.600 peak 20612	resid 83 and name 0.800 peak 20702	4.	resid 56 and name resid 54 and name 7.000 peak 20782	1d 62 and name 1d 62 and name 2.400 peak 20822
1.700	gid 'BrD ' and re	2.100	1914 "BrD " and re 1914 "BrD " and re 300 4.900	19142} *gid *BrD * and re *gid *BrD * and re	3.900	81d *BrD * and re 81d *BrD * and re 600 1.700	(9852) 19id 'BrD ' and re	4 '8r0 ' and re	segid 'BrD ' and re segid 'BrD ' and re	12} d "BrD " and re	3.100 2.400	6. 4nd	gid "BrD " and rec gid "BrD " and rec 3.800	ěě	d BrD and res	d BrD and red	3.5	eegid "BrD " and res eegid "BrD " and res 2.600 1.700 (2042)	d BrD and res	2.2	eegid BrD and resegid BrD and res	2 2		amgid "BrD " and res amgid "BrD " and res 1,400 0 500 {20772}	Pegid 'BrD " and res Segid 'BrD " and res 3.400 2.900	megid "BrD " and res megid "BrD " and res 3.800 2.000 [20482]	"BrD" and res 2.400
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4.476	7.316	6.193	. 6.193	7.315	3.163	2.325	1.479	3.162	4.474	99.166	5.745	7.259		3.146	5.367	5.542	¥.00.4	1.645	1.571	7.606	7.414	4.163	
2.634 ppm2	3.177 pps2	3.177 ppm2	2.634 ppm2	2.634 ppm2	2.641 ppm2	1.699 ppm2	2.641 ppm2	1.501 ppm2	2.340 ppm2	4.459 ppm2	1.747 ppm2	1.751 ppm2	1.747 ppm2	1.056 ppm2	1.056 ppm2	1.056 ppm2	0.740 ppm2	1.155 ppm2	1.155 ppm2	2.634 ppm2	2.634 ppm2	2.634 ppm2	
0.10111K+03 ppm1	0.11575G+02 ppm1	0.30\$41B+02 ppm1	0.54284K+02 ppm1	0.91289K+02 ppml	0.717088+02 ppm1	0.10075E+03 ppml	0.20830E.03 ppm1	0.87215E+02 ppm1	0.13858E+03 ppm1	0.662448+01 ppm1	0.54169E+02 ppm1	0.90841£+01 ppm1	0.97356£+01 ppm1	0.56657E+02 ppm1	0.44267E+03 ppm1	0.15411K+03 ppm1	0.249838+03 ppm1	0.14668E+03 ppm1	0.37404K+03 ppm1	0.48521E+02 ppm1	0.55049E+02 ppm1	0.31537&+02 ppm1	
	volume	volume	volume	volume	volume	volume	volume	volume	volume	volume	volume	volume	volume	volume	volume	volume	volume	volume	volume	volume	volume	voluma	
0.11000E+01 volume	0.110006+01	0.11000E+01	0.11000\$+01	0.11000E+01	0.110008+01	0.110006+01	0.110006.01	0.110008+01	0.110008+01	0.110006+01	0.110006+01	0.11000E+01	0.110508+01	0.110005+01	0.110006+01	0.11600E+61	0.11000£+01	0.110006+01	0.11000E.01	0.110006+01	0.110005+01	0.11000E+01	
name MD2 }} name HA }} 20692 weight	name HD3)) hame HE%) 20902 weight	and name HD1 }} and name HDb } peak 20912 weight	name HD2 }) name HD%) 20922 weight	neme HDZ }} neme HEV } 20912 weight	name HB1 }} name HD1)} 20952 weight	name HB2 }} name HG1 }} 20962 weight	name HG2 }) tame HB1 }} 20972 weight	name HG2)) name HD1)) 21012 weight	name HG1)) name HA)) 11022 weight	name HA)) name HG2)) 11162 weight	name HB)) name HDV)	name HB)) name HEt) 21522 weight	name HB }} name HE' } 21532 weight	name HG1%) Came HB2 }} 21602 weight	name HG1%) name HA }) 21622 weight	name HG1%) name HA)) 21632 weight	name HG2%) name HA)) 11762 weight	name HD14) name HG14) 21832 weight	and name KD1v) and name HG2v) ask 21642 weight	and name HB)) and name HD') tak 21852 weight	name HB)) name HEt) 31862 weight	name HB)) name HA)) 21872 weight	and name HD14)
and name and name peak 20692	and name and hame	Pe and	and name and name	and name and name peak 20932	and name and name	and name and name	and name and tame peak 20972	and name and name peak 21012	and name and name peak 21022	and name and name peak 21162	and name and name	and name and name	and name and name peak 21532	and name and name peak 21602	and name and name peak 21622	and name and name	and name and name	and name and name	ă.	Δ.	and name and name peak 21862	and name and name peak 21872	
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2.603	2.73	3.028	3.272	3.606		4		3		7.28					38.	7.418	7.604	5.163	4.367	4.972	5.134	5.031	6.477
1.155 ppm2	1.155 ppm2	1.155 ppm2	1.155 ppm2	1.155 ppm2	1.155 ppm2	1.155 pon2	1.797 pond	1,006 poss	1.007 0082	1.007 ppm2	1.00.1	1.007	1.006 ppm2	0.409	1,427 10083	1.646 ppm2	1.646 pon2	2.880 ppm2	2.537 ppm2	3.610 ppm2	4.114 ppm3	2.615 ppm2	2.635 ppm2
0.24085E+03 ppm1	0.369018+03 ppm1	0.32396E-03 ppm1	0.228428+03 ppm1	0.28478E+03 ppm1	0.191538+03 ppm1	0.57384E+03 ppm1	0.99146E+02 ppm1	0.46395E+03 DDM1	0.30083E+02 ppm)	0.12510E+02 ppm1	0.31318E+03 ppm1	0.147548+03 ppm.1	0.30274E+03 ppm1	0.57888\$*02 ppm1	0.43395E+02 ppm1	0.52744E+03 ppm1	0.29406E+03 ppm1	0.11329E+03 ppm1	0.531088+03 ppm1	0.98321K+03 ppm1	0.81098E+02 ppm1	0.28012E+03 ppm1	0.17156E+02 ppm1
1.11000E-01 volume	0.11606£+01 volume).11600E-61 volume	0.11000K+81 volume	0.11000E+01 Volume	0.11040E+01 volume	0.11000E+01 volume	0.11000E:01 volume	0.11000E+01 volume	0.11000E+61 volume	0.11000E+01 volume	.11000E-01 volume	.11000E+01 volume	0.11000E+01 volume	0.11000E+01 volume	0.11000E+61 volume	.11000E-01 volume	0.11000K+01 volume	0.11000K+01 volume	.11000K-01 volume	0.11000E+01 Volume	0.11000E+01 volume	0.11000E+01 Volume	3.11000K+81 volume
and name HB2)) peak 21912 weight (and name MD14) and name MB1)) peak 21922 weight (and name HDI4) and name HGI }} peak 21932 weight (and name HB1) and name HB2)) pask 21942 weight	and name HB1) and name HB1) peak 21962 weight	and name HD14) and name HA)) peak 21992 weight (and name HD14) and name HA)) peak 22002 weight (HOZA) HDA) weight	HG24) HEV)	and name MO2V) and name HEV)	and name MG24) and name HA)) seak 22172 weight o	HG21) HG21) weight	H012)) HA))	H024) HA))	and name HO1%) and name HE%) mak 22512 weight o	and name HOI%) and name HD%) peak 22522 weight o	and name HG1 }) and hame KA)}	and name HB1)) end name HA)) eak 22792 weight 0	and name HEL)) and name HA)) peak 22872 weight o	and name HD2)) and name HA)) mak 22942 weight 0	and name HO1 1) and name HA 1) mak 23162 weight o	and name Mdl 1) and name HA 1) wak 23172 weight 0
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1.090	0.928	3.525	3.535	4.508	4.507	.693	4.378	4.370	3.074	4.753	2.53			9				1 5	95		4.947	4.947	7.708
1.434 ppm2	3.494 ppm2	1.989 ppm2	2.290 ppm2	1.894 ppm2		3.124 ppm2	3.469 DD#2	3.076 ppec	4.784 ppm2	3.917 ppm2	1.797 page 1	1.599 Don2	1.155 poss	25.1					1.00	1. 893 ppm2	2.519 ppm2	2.596 ppm2	3.129 ppm2
0.193595+03 ppm1	0.20841E-01 pm1	0.200668+02 ppm1	0.655\$78+02 ppm1	0.12763E+03 ppm1	0.50116E+03 ppm1	0.91712E-02 ppm1	0.67606E+02 ppm1	0.26410K+03 ppm1	0.62910E+03 ppm1	0.679298+02 ppm1	0.55437E+03 ppm1		0.51046E+02 ppm1		117158-01	0.314148.03	100000000000000000000000000000000000000	0.202268.03 0083	0.14101E-04 ppm1	0.62174E-03 ppm1	0.45243E+02 ppm1	0.23440E+02 ppm1	0.1485E+03 ppm1
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and name peak 24662	and name and name pack 24672	and name and name pask 24742	and name and name peak 24752	and name and name peak 24762	and name and name peak 24812	and name and name pack 24872	and name and name peak 24902	and name and name peak 24912	and name and name peak 24932	resid 85 and name resid 82 and name 2.400 peak 35433	resid 101 and name resid 101 and name 1.300 peak 2552	resid 21 and name resid 18 and name 2.200 peak 25612	resid 110 and name resid 75 and name 2.100 peak 26032	resid 110 and name resid 18 and name 1.100 peak 26172	resid 110 and name resid 18 and name 2.200 peak 26182	resid 116 and name resid 116 and name 1.600 peak 26102	resid 103 and name resid 106 and name 2.400 pesk 26562 a	reeld 101 and name resid 100 and hame 1.800 peak 26592 v	and 103 and name aid 103 and name 1.000 peak 26642	resid 103 and name resid 103 and name 1.200 peak 26652	resid 103 and name resid 100 and name 2.000 peak 26662	and name and name peak 26672	and name and name pack 26722
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med forms (81) med fo	resid 94 and name resid 32 and name 3.200 peak 26792	and but	Weight	0.110006.01	0.11000E+01 volume 0.11000E+01 volume	0.35916E+03 ppm1 0.10089E+03 ppm2	2.733 ppm2	7,998
10 10 10 10 10 10 10 10	resid 94	and name	HG1))				1.123 ppm2	2.711
1.112 pm.2 1.112 pm.2 1.112 pm.2 1.112 pm.2 1.112 pm.2 1.113 pm.2 1.111	resid 67	and name and name eak 26892	HB1)) HO1))				2.779 ppm2	3.021
1, 11, 11, 11, 11, 11, 11, 11, 11, 11,	resid to	and name and name and name and name	45 45 55 55 55 55 55 55 55 55 55 55 55 5				3.812 ppm2	4.678
100 1 1 1 1 1 1 1 1	1.700 p resid 77 resid 74 2.000 p	and name	HB1 1)				3.962 ppm2	4.376
1,000 1,00	resid so resid so 2.100 p	and name and name sek 27242	HB2))				2.536 ppm2	3.955
(811) (811)	resid so resid so 2.000 p	and name and name	KB2)) HD2)) weight	0.11000E+01 .		0.14981E+03 ppm1	2.536 ppm2	3.890
Maright 0.11000E-01 volume 0.72272E-02 ppm1 3.979 ppm2 might 0.11000E-01 volume 0.91001E-02 ppm1 1.059 ppm2 might 0.11000E-01 volume 0.91001E-02 ppm1 1.899 ppm2 might 0.11000E-01 volume 0.7012E-02 ppm1 1.899 ppm2 might 0.11000E-01 volume 0.7012E-02 ppm1 1.899 ppm2 might 0.11000E-01 volume 0.1367E-02 ppm1 1.600 ppm2 might 0.11000E-01 volume 0.1367E-02 ppm1 1.449 ppm2 might 0.11000E-01 volume 0.49710E-02 ppm1 1.449 ppm2 might 0.11000E-01 volume 0.1050E-02 ppm1 1.351 ppm2 might 0.11000E-01 volume 0.485E-02 ppm1 1.351 ppm3 might 0.11000E-01 volume 0.485E-02 ppm1 1.	resid 56 resid 34 0.000 ps	and name and name ak 27312	Ho Ho	0.11000E+01 1			2.33e ppez	5.842
1.034 ppmal (1021) (1.200 p	and name	1616 1617 1617 1617 1617 1617 1617 1617				2.979 ppm2	. 990's
MAN 19 1 1.59 ppm2 manifest co. 11000E-01 volume 0.7013E-03 ppm1 1.599 ppm2 manifest c.11000E-01 volume 0.12667E-03 ppm1 1.600 ppm2 manifest c.11000E-01 volume 0.13776E-02 ppm1 0.760 ppm2 manifest c.11000E-01 volume 0.49710E-02 ppm1 0.662 ppm2 manifest c.11000E-01 volume 0.49710E-02 ppm1 1.513 ppm2 manifest c.11000E-01 volume 0.25930E-02 ppm1 1.353 ppm2 manifest c.11000E-01 volume 0.4845E-02 ppm1 1.353 ppm2 manifest c.11000E-01 volume 0.4845E-02 ppm1 1.354 ppm2 manifest c.11000E-01 volume 0.6853E-02 ppm1 1.354 ppm3 manifest c.11000E-01 volume 0.6853E-02 p	2.400 pa resid 22 resid 22	and name	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1			0.93003E+02 ppm1	1.05e ppm2	4.106
### 10000000000000000000000000000000000	resid 22 resid 22 1.200 pr	and name and name sak 27522	KD24) KB2 J)				1.599 ppm2	2.286
Miles Mile	resid 73 resid 73 2.100 pe	and name and name ak 27682	HB2)) Weight				1.600 ppm2	2.483
1,1000E-01 volume 0.49710E-02 ppml 0.662 ppml 0.662 ppml 0.1000E-01 volume 0.49710E-02 ppml 0.662 ppml 0.1000E-01 volume 0.49710E-02 ppml 0.11000E-01 volume 0.25920E-02 ppml 0.11000E-01 volume 0.25920E-02 ppml 0.131 ppml 0.11000E-01 volume 0.4645E-02 ppml 0.135 ppml 0.11000E-01 volume 0.6623E-02 ppml 0.134 ppml 0.11000E-01 volume 0.6623E-02 ppml 0.134 ppml 0.11000E-01 volume 0.6623E-02 ppml 0.1000E-01 volume 0.6623E-02 ppml 0.1000E-01 volume 0.6623E-02 ppml 0.1000E-01 volume 0.6633E-02 ppml 0.1000E-01 volume 0.6633E-02 ppml 0.1000E-01 volume 0.6633E-02 ppml 0.1000E-01 volume 0.6833E-02 ppml 0.1000E-01 volume 0.10	resid 78 resid 82 1.900 pe	and name and name ak 27922	KD14) KD1) weight				0.760 ppm2	7.259
High	resid 78 resid 82 2.100 pm	and hame and hame ak 27972	KD24) KD4)				0.662 ppm2	7.259
HEATA) MAX 1) MAX 1) HEATA 1) HAATA 1) HAATA 1,1000E-01 Volume 0.005138-02 ppm1 1.302 ppm2 weight 0.11000E-01 Volume 0.005138-02 ppm1 1.302 ppm2 weight 0.11000E-01 Volume 0.005138-02 ppm1 1.302 ppm2	resid S6 resid 34 2.200 pe	and name and name ak 28242	ND14) HB1))	0.11000E+01 w			1.549 ppm2	4.110
HERT) HERT) HERT 1) HE	resid 56 resid 34 1.700 pe	and name and name ak 28282	HD24) HA)) weight	0.11000E+01 v			1.253 ppm2	5.540
MED 1) MED 1) MED 2) MED 2) MED 3) ME	resid 56 2.100 pc	and name and name	HB1)) weight	0.11000E+01 v			1.253 ppm2	4.110
HD1) HA }) Weight 0.11000Er01 volume 0.485198401 ppml 1.303 ppml	resid 56 resid 34 2.300 p	and name and name	HD26) HB2 1)				1.254 ppm2	3.134
	asid 102 asid 102 1.100 pe	and name and name ak 28672	HD10)				1.303 ppm2	4.262

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	0.401825.63 ppm1	0.17484K•01 ppm1	0.64530E+02 ppm1	0.44730E+03 ppm1	0.12060E-03 ppm1	0.16180E+03 ppm1	0.45332E+02 ppm1	0.36619E+02 ppm1	0.693456+02 ppm1	0.26299R+03 ppm1	0.15191R+03 ppm1	0.46894E.03 ppm1	0.20014E+02 ppm1	0.20564E+03 ppm1	0.23040E+03 ppm1	0.23393R+03 ppm1	5.221246+03 ppm1	1.072748+02 ppm1	3.452878+02 ppm1	0.39658E+03 ppm1	0 49260K+03 ppm1	0.18736E+03 ppm1
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\$.000 ppm2

0.32594E+02 ppm3

2.799

4.755 ppm3

0.31695E+02 ppm1

4.65

5.099 ppm2

0.78869E+01 ppm1

1.433

1.889 ppm2

0.91996E+02 ppm1

2.311

4.509 ppm2

0.67300£+03 ppm3

4.509 ppm2

0.18352E.03 ppm1

1.4

\$.541 ppm

0.99741E+02 ppm1

0.10000E.01 volume

2.597

4.360 ppm2

2.345

1.522 ppm2

0.15368E.02 ppm

1.51

2.980 ppm2

0.19616E-03 ppm1

1.339

4.907 ppm2

0.349578+02 ppm1

vol une

1.320

4.510 ppm2

4.460

3.080 ppm2

0.147878+03 ppm1

volume

0.10000E+01

1.587

2.334 ppm2

0.46116E+02 pgm.1 0.90515E+02 pgm.1

2.876

2.291 ppm2

...

2.979 ppm2

0.16032E-03 ppm1

2.571

5.347 ppm2

0.437138+02 ppm1

volume

0.10000E+01

3.33

0.761 ppm2

2.467

3.288 ppm2

0.18992K+02 ppm1

I reald 54 and name M I reald 59 and name H I. 500 peak 12502 w I reald 59 and name M I reald 77 and name H I. 600 peak 12532 w

1.331

1.648 ppm3

0.10000E+01 volume

1 reeld 71 and name N 1 reeld 18 and name N 1 800 peak 13732 w

1.0

4.608 ppm2

0.29522E+02 ppm1

60, 0

4.607 ppm2

0.10000E+01 volume 0.66213E+02 ppm1

and name and name peak 12752

5.143 5.143 0.730	2.316	1.417	1, 996 1, 410 2, 500 1, 159	4,443 1,010 0,480 1,132
3.486 ppm2 3.486 ppm2 3.583 ppm2 3.275 ppm2 4.607 ppm2	1.548 ppm2 1.648 ppm2 1.795 ppm2	2.634 ppm2 2.634 ppm2 2.537 ppm2 5.296 ppm2	1.458 ppm2 4.551 ppm2 1.446 ppm2 4.656 ppm2 3.665 ppm2	3.636 ppm2 1.425 ppm2 1.429 ppm2 5.238 ppm2
			02 ppm 1	-02 ppm1
na 0.51446E-03		0 0.18896E+02	_	0.360158+03 0.356886-03 0.143558+01
0.100008.01 volume 0.100008.01 volume 0.100008.01 volume 0.100008.01 volume	0.10000£.01 volume 0.10000£.01 volume 0.10000£.01 volume	0.100005.01 volume 0.100005.01 volume 0.100006.01 volume		0.100006.01 volume 0.100006.01 volume 0.100006.01 volume
	MO11) MO12) MO12) MO13)			
and name and name pask 13092 and name and name and name and name and name pask 13122 and name	resid 55 and name N resid 55 and name N resid 116 and name N resid 116 and name N resid 55 and name N resident 55 and name N r	and name k		and frame HG and frame HG and frame HG and frame HG pack 13972 we and frame HG and frame HG
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	2.34	5.362	1.967	4.93	2.136	3.541	3.310	4.437	1.316	3.65	90.1	1,438	2.0	2.181		;		1.27	2.351	3.65	5	1.078	
4.360 ppe.2	2.091 ppm2	1.402 ppm2	4. 655 ppm2	3.667 ppm2		4.457 ppm2	6.000 pm2	2.289 ppm3	2.334 ppm2	1.486 ppm2	3.769 ppm2		4.606 ppm2	4.411 ppm2				1.949 ppm2	3.866 ppm2	1.057 ppm2	rudd cor:	2.535 ppm2	s. etc ppm3
0.36366E+02 ppm1	0.17944E+03 ppm1	0.21486E+03 ppm1	0.421778+02 ppm1	0.3251K+02 ppm1	0.54061K+02 ppm1	0.103356.03 ppm	G. 6.13708: U. J. Plent	0.10\$86K+03 ppm1	0.49515E+00 ppm1	0.30120K+03 ppm1	0.41084E+03 ppm1	0.19913E-02 ppm1	0.25435E+02 ppm1	0.14014E+03 ppm1		0.21487E-01 pres			0.30202E+02 ppm1	o strankeda ppm.		0.28669E+02 ppm]	
0.10800E.01 volume	0.10000£.01 volume	0.10000E.01 volume	0.10000E.01 volume	0.100005.01 Volume	0.10000E+01 volume	0.10000E+01 volume	U.10000K+U1 vulume	0.10000E-01 volume	0.10000£+01 volume	0.10000E+01 volume	0.10000E+01 volume	0.10000E.01 volume	0.10000K+01 volume	0.10000E.01 volume		0.10000£.01 volume	80000			100005.01		TOOOGE OF ACTUME	1.10000E+01 volume
68 and name HB2 }) 00 peak 13862 weight	resid 76 and name MBN) resid 80 and name MGI)) 2.000 peak 14012 weight	resid 14 and name HD11) resid 70 and name HA 1) 1.800 peak 14052 weight	113 and name HA)) 113 and name HBt) 00 peak 14112 weight	eid 96 and name MB2 }) eid 30 and name MB1 }) 1.600 pesk 14212 weight	99 and name HA)) 102 and name HG)) 00 peak 14222 weight	resid 99 and name MA)) resid 62 and name HB2)) 2.200 peak 14242 weight	31 and name HA) 32 and name HO2) 50 peak 14363 weight.	eid 31 and name HBN) eid 35 and name HA)) 2.200 peak 14272 weight	resid 110 and name NB resid 115 and name HD14 0.000 peak 14292 weight	resid 53 and name HD24) resid 22 and name HB1)) l.600 peak 14302 weight	103 and name HA)) 102 and name HB2)) 30 peak 14332 weight	resid 106 and name HA)) resid 109 and name HG1)) 1.500 peak 14152 weight	sid 15 and name HA)) sid 14 and name HG))- 1.700 peak 14382 weight	eid 110 and name NA)) eid 115 and name HB1)) 2.000 peak 14442 weight	110 and name HA))	resid 110 and name HG28) resid 115 and name HD18} 1.700 peak 14452 weight	11 and name HG1)) 10 and name HG2s) 0 thenk 14512 (month)	and name KA)) and name HG11)	and name MD14) and name MO))	and name HD1%) and name HD2%)	and name HEA] and name HOAN)	and name	and name and name pask 14782
egid "BrD " end resid (5.600 3.200 1.90	egid BrD and resid egid BrD and resid to 2.000 2.000 2.00	eegid "BrD " and resid ; 2.700 1.800 1.800 1.412	Megid BrD and resid 14 megid BrD and resid 113 2.400 2.400 142121	megid BrD and resid seed 30 megid BrD and resid 30 1.000 1.000 1.000	medid "BrD" and resid 99 agid "BrD" and resid 102 agid 104 2.400 2.900 2.100 per	eegid 'erD ' end reald seegid 'erD ' and reald s 3.000 2.200 2.20 [14262]	segid 'BrD ' and resid 33 segid 'BrD ' and resid 33 3,300 3,700 2,300 per		aegid BrD " and resid 1 aegid BrD " and resid 1 5.500 5.500 0.00 (14302)	megid "BrD " and resid a megid "BrD " and resid 2 2.500 1.600 1.60	eegid "BrD" and resid 103 a segid "BrD" and resid 102 a 3.500 3.100 2.000 pea	egid BrD and resid 1 egid BrD and resid 1 .000 4.000 1.50		2 2	eegid BrD and resid 110 eegid BrD and resid 115 [14652]	agid "BrD " and resid 1 agid "BrD " and resid 1 .600 1.700 1.70	14512} *egid *BrD * and resid 111 *egid *BrD * and resid 110 ***********************************	[14652] megid "BrD" and resid 18 megid "BrD" and resid 21 3.700 3.400 1.800	(14672) megid "BrD " and reald 18 megid "BrD " and reald 63 3.100 2.400 2.400		{14752} ecgid "BrD " and reald 54 ecgid "BrD " and reald 61 3.700 3.400 1.800	2.2	14782 820 and resid 36 eegid "BED" and resid 57 1300 1.300 1.300 [15012]
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~~ (• • ~ ~ •	4.900 (16412)	4.700 (16492)	2.200 (16502)				1166	6.300 6602))(segid ASSI (16792)(segid)(segid	2.700 {16842} eegid *B	2.200 (1688 begid	6862	(16892 8691d 8691d 2,200	(16902) eegid "Bi	(16932 segid segid 5,500	(1697) 8091d 8091d	(17032) segid "B segid "B 2.400	(17072) eegid 'BrD eegid 'BrD 3.800	(17192) eegid "		(segid '8rD (segid '8rD (segid '8rD 1.900) R [r7352 } (segid '9rD (segid '9rD
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																						متد
10.02	***			2.312	1.63	1.474	3.200	2.206	1.897	2.540	7.627	3.900	1.652	.022	2.367	6.998	1.146	3.149	2.883	2.884	2.605	1.571
3.275 DD@2	3.276 ppm2			3.374 ppm2	3.572 ppm2	3.572 ppm2	3.572 µm2	3. 6 72 ppm2	3.573 ppm2	3.670 ppm2	3.673 ppm2	4.606 ppm3	3.815 ppm2	3.670 ppm2	5.148 ppm2	3.522 ppm2	1.669 ppm2	3.522 ppm2	3.669 ppm2	3.522 ppm2	3.522 ppm2	4.999 ppm2
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0.200558+02 ppml	1. ppm1	60.0		K-03 ppm1		E+02 ppm1	K+03 ppm1	K+03 ppm1	E-02 ppm1	18+02 ppm]	f.03 pps)	E+02 ppm3	E+02 ppm1	E+03 ppm1			R-01 ppm1	S+03 ppm1	E+02 ppm1	E+02 ppm1	E+02 ppm1	E-02 ppm1
. 2005	0.963658+01	0.300016.00		0.15966	0.196038+03	0.11011E+02	0.10881K+03	0.12753E+03	0.31328E.02	0.869578+02	0.637468+03	0.673338+02	0.19033E+02	0.261676+03	0.30931E+02	0.38285£+02	0.900008+01	0.436255+03	0.357248+02	0.44106E+02	D.16622E+02	0.712768+03
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HB1 1) HG14) weight	KB1)) KD4)	HDA)	HG2V)	HB2 ;)	HB2))	KB1)) KG2))	182	HBI)	KB2 1) HB2 1)	HB1)) HG2)) weight	NB1)) ND4)	### ##################################	HB1)) HD14) weight	ИВ1)) ИZ)) weight	KG 11	HB2)) KD4)	KDI)	KB2)) HD1)) weight	HB1)) HB1))	HB2)) HB1))	ивз !) ивз !) veight	HA)) HG24) weight HB1))
		DAME H	Define H	name H	name H name H 5182 v	Dam K	H 4044	7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	SSS 4	Pare H	N STILL	4 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5		name KB name KZ 15932 we	name H name H 6052 v	Dame H	name H	Dame K	name Hi name Hi 6132 ve	name Hi	Dame H	Tame H
and name and name peak 15012	and name and name peak 15032	and name and name peak 15042	and name and name peak 15052	and name and name peak 15092	and name and name peak 15162	and name and name peak 15192	and name and name peak 19402		# # # # # # # # # # # # # # # # # # #	F 5 5 4	1	and name and name beard name	and name and name peak 15882	334	and name and name peak 16052	1 2 4	and name hand name h	and name and name peak 16122	and name and name peak 16132	and name and name peak 16152	and name and name pask 16162	and name and name peak 16213 and name
	* 7 8	1.300	resid 46	2.000 2	resid 67 resid 62 1.500	resid 67 resid 62 1.100	1.200	resid 95 and name 2.100 peak 15412 v	resid 82 and name F resid 103 and name F 1.800 peak 15552 v	reeld 107 and name is reeld 103 and name it 2.400 peak 15592 v	resid 107 and hame P resid 107 and name P 1.200 peak 15712 v	2.200	See 2 and resid 15 and name gid "BrD" and resid 63 and name 000 4.000 1.500 peek 15883	resid 42 and name resid 107 and name 1.700 peak 15932	1.500	bound and resid as and resid as and resid 14 3.200 3.200 3.900 p	sgid "BrD" and resid 68 agid "BrD" and resid 63 6.50 6.50 1.000 p	2.000	egid "BrD" and resid 6s egid "BrD" and resid 63 .600 3.200 1.900 p	gid BrD and resid 68 gid BrD and resid 63 gid BrD 3.100 2.000 p	1.400 1.400	resid 49 2.300 resid 93
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BrD . and	BrD • and BrD • and 4.500	BrD * enc	E E	BrD and BrD and 2.000	162) id "BrD " and id "BrD " and 00 4.000	1d 'BrD and 1d 'BrD and 10 4.400	1d 'BrD and 1d 'BrD and 00 3:300	id "BrD " and 00 2.100 552}	1d "BrD " and 1d "BrD " and 00 3.400 592]	1914 BrD and r 1914 BrD and r 100 2.400	id BrD and 114 BrD and 1.200	BrD * enc 3.700	0.0	1d BrD and 1d BrD and 1.700	org.	2 2	. or 6	Bro Bro	0.0	egid BrD and egid BrD and 1500 3.100	870 - en	eegid 'BrD and r eegid 'BrD and r 3.200 2.600 [16112] eegid 'BrD and r eegid 'BrD and r
. 000		ASSI (15042) ((eegid (aegid)	15052) egid 1	15092} egid 'i	15162 1000 1000 1000	916 916 1400 15402	000 T	. 900 15552}	#91d . #91d . . 700 15592]	egid .	9 gd 200	916 916	000 000 000	p 16.	4914 °	egid . 600	egid . 500	916 916 500 1500	P 100	93.d 93.d 500	egid Bri egid Bri .100	#914 *
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3.337

.006 ppm2

0.10000E.01 volume

2.209

3.125 ppm2

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volume

2.819

5.589 ppm2

0.11894E+02 ppm1

Volume

4.995

3.375 ppm2

0.22670E+03 ppm1

4.6

3.677 ppa2

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7.039

4.557 ppm2

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0.10000E+01 volume

7.511

1.556 ppm2

0.10000E+01 volume

0.100008+01 volume

0.10000E+01 volume

7.634

1.554 ppm2

5.44

4.804 ppm2

7.053

3.676 ppm2

į

0.10000E+01 volume

3.576

4.462 ppm3

volume

7.790

4.462 ppm2

volume

HN2))

4.903 ppm2

0.433238+03 ppm

volume

7.719

4.407 ppm2

ã

volume

1.319

1.127 ppm2

0.22025E+02 ppm1

0.10000E+01 volume

1.495

3.522 ppm2

1.562

3.621 ppm2

1.645

3.620 ppm2

0.72449E+01 ppm1

4.802

4.409 ppm2

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0.16000E+01 volume

4.409 ppm2

7.496

0.47079E+02 ppm1

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4.114 pres	t	3.122 00		0.759	0.761 ppm	0.763 pp	0.760 ppm2	0.859 pq	0.859 pp	0.859 pp	0.324 pp	2.783 99	2.190 pp	1.055 ppm2	-0.176 pp	-0.174 pps2	3.524 ppm2	3.227 ppm2		3.226 ppm2	3.226 ppm3		3.522 ppm2
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					۰						0.53	0.42		0.26		0.30		0.289		0.10			
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005.01		0.100008+01	0.10000E+01	0.100008.01	0.100005.01	0.100006+01	0.100006.01	0.100006+01	0.100005+01	0.10000E+01	0.100005.01	0.100008+01	.100008.01	0.100002+01	0.100006+01	0.100005+01	0.100008+01	0.100008+01		0.10000\$+01	0 6. 01		306.01
		0.100	0.100	0.100	0.100	0.100	0.100		0.100	0.100	0.100	0.100	0.100	0.100	0.100	0.100	0.1000	0.1000		0.1000	0.1000		0.100
HB1)) HD1V)	HB1)	HE 1)	# 19 m	HG24) KZ)) weight	HO21) HD1)	HG2() KD()	HG24) HEA) weight	HG1)) HA))	HG1)) KB1)) we1ght	HB1)) HB2)) weight	HG2)) HA)) weight	HD1)) HB4)	KD2)) KD4)	KB1)) KA)) waight	KB2)) KA)) weight	HB2)) HD4) weight	HO1))	KO1)) KB2)) weight	KG2 1)	HG2)) HD14)	MG2)) MD14) weight	HO1 ;	HO1)) HB1))
		and name and name peak 17452	and name and name peak 17502		0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	and hame and hame peak 17632	and name and name peak 17642	and name and name peak 17712	name name 17732	and name hand name hand name h	and name and name and name l		neme 1 neme 1 17902	name 1	and name and name peak 17962	name name 17982	name name 18012	1000		Dame 1	10113	4	name name 18122 :
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2.507

2.092 ppm2

0.10000E+01 volume 0.21436E+03 ppm1

1.76

2.092 ppm2

0.32487E+03 ppm1

0.10000£.01 volume

1.963

2.092 ppm2

0.15327E+03 ppm1

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1.432

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0.350208.02 ppm3

0.10000E.01 volume

6.143

1.500 ppm2

0.16681E+03 ppm1

0.10000£+01 vulume

2.337

4.656 ppm2

0.95067E+02 ppml

0.10000E+01 volume

7.903

2.190 ppm2

0.65240E+03 ppm1

0.10000E+01 volume

0.10000£+01 volume

7.701

2.190 ppm2

7.259

2.190 ppm2

0.10060E+01 volume 0.16019E+03 ppm1

5.005

2.190 ppm2

0.92786E+02 ppm1

0.10000E+01 volume

4.94

3.190 ppm2

0.10441E+03 ppm1

0.10000E+01 volume

2.613

2.190 ppm2

0.10256E+03 ppm1

0.10000E+01 volume

2.784

2.092 ppm2

0.45000K+02 ppm1 0.26558E+03 ppm1

0.100008+01 volume

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7.901

4.459 ppm2

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4.457 ppm2

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4.950

4.458 ppm2

0.10000E+01 volume

1.922

4.458 ppm2

0.24667E+03 ppm1

volume

1.222

4.903 ppm2

0.100002.01 volume

3.670

4.903 ppm2

0.10000E+01 volume 0.48759E+02 ppml

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0.575908+02	0.37691E	0.744386	0.245538+03	0.295666.03	0.42	0.123936+02	0.157688	0.65857E+03	0.35		9.6	0.61439E+03	71.0	0.54	0.176808	0.42	2.	0.52	.62	.7	9.14	6.4	97.0	
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4.804 ppm2	4.804 ppm2	4.013 ppm2	4.015 ppm2	3.620 ppm2	3.916 ppm2	3.670 ppm2	3.620 ppm2	3.917 ppm2	1.551 ppm2	1.549 ppm2	1.599 ppm2	1. 599 ppm2	1.599 ppm2	1.599 ppm2	1.548 com2	2,334 pons			254 2000			1.155 ppm2	1.184 ppm2
0.667726+02 ppm1	0.303168+02 ppm1	0.12678E+03 ppm1	0.62906E-02 ppm1	0.295346+03 ppm1	0.15410R+03 ppm1	0.12121K+03 ppm1	0.45042£+03 ppm1	0.32323K+03 ppm1	0.41073E-02 ppm1	0.10658E+03 ppm1	0.38225E+02 ppm1	0.38422£+02 ppm1	0.202668+02 ppm1	0.18743E+03 ppm1	0.8446BE-02 ppml	0.55301E+03 pgm1	0.198968.02 prest		0.149608.02 Hpm1	0.71378E+02 ppm1	0.29658E.03 ppm1	0.22034E+03 ppm1	O.Billsk-Ol ppml
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	0.33522E+03 ppm1	0.26306K-03 ppm1	0.22393E+03 ppm1	0.44296E+02 ppm1		36066K-01 ppm1	0.56268803 pm1	1.115178+03 ppm1	0.31951E+02 ppm1	0.597516+02 ppm1	0.182498+02 ppm1		0.18330E+02 ppm1	0.20958E+03 ppml	0.4900\$E+02 ppm1	0.85246E+02 ppm1	0.16098E+02 ppm1	0.47687E+02 ppm1	0.23078E+02 ppm1	0.49600E+02 ppm1	0.669376+02 ppm1	0.24126E+02 ppm1	0.46123E+02 ppm1	
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0.80321E+02 ppm1

1.36

1.847 ppm2

0.36305E+02 ppm1

volume

3.002

1.646 ppm2

0.23714£.02 ppm1

0.10000E+01

4.516

1.847 ppm2

0.98620E+01 ppm1

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2.536 ppm2

0.405578+02 ppm1

2.88

2.536 ppm2

volume 0.17311E+03 ppm1

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0.12717E+03 ppm1

0.10000E+01 volume

1.863

2.535 ppm2

0.105586+03 ppm1

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7. 111

4.361 ppm2

0.67859E-02 ppm1

0.100005+01

5.010

2.179 ppm2

0.322108+02 ppm1

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1

2.731

5.000 ppm2

0.83013E-02 ppm1

0.10000E+01 volume

2.73

5.003 ppm2

0.67723E+02 ppm1

0.10000E-01 volume

1.90 1.337

0.13311E+02 ppm1

0.10000E+01 volume

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5.445 ppm2 4.804 ppm2

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4.808 ppm2

0.60630E+02 ppm

1.604

4.507 ppm3

0.72004E+02 ppm1

3.077

4.607 ppm3

0.53302R+02 ppm1

0.10000E+01 volume

4.550

\$.000 ppm2

0.14178E+03 ppm1

0.10000E.01 volume

2.463

0.85748E+02 ppm1

0.10000E.01 volume

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3.42

4.755 ppm2

4.550

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0.10000E+01 volume 0.51818E+01 ppm1

2.453

5.346 ppm2 4.360 ppm2

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2.536 ppm2

7.486

2.289 ppm2

0.75523E+02 ppm1

volume

0.10000E+01

4.616

2.486 ppm2

0.10000E+01 volume 0.51425E+03 ppm1

7.487

2.388 ppm2

0.10000E.01 volume

1.96

388 ppm2

0.89147E+02 ppm

volume

0.100005.01

7.421

5.758 ppm2

Volume

0.11000E+01

7.261

5.758 ppm2

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vol use

7.261

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6.688 ppm2 5.758 ppm2

volume

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6. 685 ppa.2

4.533

8.129 ppm2

0.110008+01 volume 0.142485+02 ppml

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6. 873 ppm2

6.874 ppm2

0.67483E+02 ppm

0.11000E+01 volume

4.67

6.872 ppm2

3.570

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0.22980E+03 ppm1

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7.780

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906	megid "BrD " and segid "BrD " and segid "BrD " and segid "500 1.700	egid 'BrD and a egid 'BrD and a .800 2:000	agid "BrD " and agid "BrD " and	9 50	P 10 0	egid "BrD " and :	200	egid BrD and egid BrD and .100 2.400	agid "BrO and r	egid BrD and a	# p p p	200	1464) megid BrD : and megid BrD : and i	1474 megid "BrD " and re megid "BrD " and re	1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	200 p. 000 p. 00	1504) segid "BrD" and r segid "BrD" and r 1,000	D169.	megid BrD and 1 megid BrD and 1 1.200 2.600	segid "BrD " and r segid "BrD " and r 2.700 1.800	eegid BrD and a	egid BrD and egid BrD and 1,700 1.800	egid 'BrD' and egid 'BrD' and 5.000 2.200
ď	4 6 ~-	- * * * - * =		22	===	- • • ~ -	- 2 2 4-	- • • ~-		- • • ~ -	322												
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1.50	7.901	3.920	1.61	4.538	3.66	1.333	1.36		3.919	1.706	3.106	2.374	2.274	1.496	2.30	1.500	1.266	0.780	1.919	3.704	7. 840	1.545	3.075
7.741 ppm2	7.719 ppm2	7.714 ppm2	7.605 ppm2	7.650 ppm2	7.646 ppm2	7.647 ppm2	7.647 ppm2		7.644 ppm2	7.616 ppm2	7.611 ppm2	7.611 ppm2	7.611 ppm2	7.539 ppe.2	7.535 ppm2	7.541 ppm2	7.529 ppm2	7.530 ppm2	7.524 ppm2	7.524 ppm2	7.513 ppm3	7.318 ppm2	7.270 ppm2
0.42209E+03 pgm1	0.35620E+03 ppm3	0.16186E-03 ppm1	0.44171E+03 ppm1	0.41516E+03 ppm1	0.17361E+03 ppm1	0.21480E+03 ppm1	.421758+03 ppm1		0.804208+02 ppm1	0.29463E+62 ppm1	0.162688+03 ppm1	0.54543E+03 ppm1	0.400488+03 ppm3	0.16991E+03 ppm1	0.10679E+03 pgm1	0.21619E-04 ppm1	0.548508+03 ppm1	0.46858E+03 ppm1	0.663168-03 ppm1	0.63063K+03 ppm1	0.62239E.02 ppm1	0.28072E+02 ppm1	0.17782E+03 ppm1
0.10000E+01 volumm 0.	0.10000K-01 volume 0.	0.10000E+01 volume 0.	0.10000E+D1 Volume 0.	6.10500K+81 Volume 0.	0.10000E+01 volume 0.	0.10000E.01 volume 0.3	.10000E+01 volume 0.		0.10000E+01 volume 0.	0.10000K+01 volume 0.:	0.100008+01 volume 0.	0.100008+01 volume 0.	0.10000E+01 volume 0.	0.10000\$+01 volume 0.	.10000E-01 volume 0.	.10000£+01 volume 0.	0.10000E+01 volume 0.	0.10000E+01 volume 0.	0.10000E-01 volume 0.	0.10000E+81 volume 0.	0.10000E+01 volume 0.	0.10000E+01 volume 0.	0.10000E+01 volume 0.
name MDt) name MD1t) 1754 weight 0.100	name MD& } name MZ 1) 1904 weight 0.100	neme KD%) neme HB1)) 1954 weight 0.100	name HD1) name HD11) 2124 weight 0.100	neme HDt) neme HA)) 2164 weight 0.100	name MEN) name MEN) 2224 weight 0.100	name NEt 3 name NB1 3) 2234 weight 0.100	name NEL) name NBL)) 2244 weight 0.100	name HEA)	name HS%) name HS1)) 2264 weight 0.100	name HEt) name HG24) 2414 weight 0.100	name HEt] name HEL]) 2484 weight 0.100	name HE%) name HG11)) 2504 weight 0.100	name NEt) name NO)) 2514 weight 0.100		name MD%) name HG11}) 2614 weight 0.100	name MDN) name MG2N) 2654 weight 0.100	name HE%) name HQ)) 2674 weight 0.100	name HEL name HDIN) 2694 weight 0.100	neme HDt) neme HB1)) 2754 weight 0.100	name HDt) name HB2)) 2774 weight 0.100	name MD%) name ME%) 2834 weight 0.100	HEL) HDIV)	name HEA) 1144 weight 0.100
resid 68 and na resid 73 and na 1.700 peak 17	resid 14. and na resid 14. and na 1.700 peak 19	seld 34 and seld 85 and 2.200 peak	seid 15 and seid 63 and 1.600 peak	seld 15 and seld 16 and 1.700 peak	send 106 and send 75 and 2.200 peak	eeld 106 and eeld 78 and 2.100 peak	esid 106 and seld 78 and 1.700 peak	esid 106 and esid 78 and	celd 106 and celd 106 and 2.100 peak	eaid 106 and eaid 17 and 1.500 peak	esid bs and 2.200 peak	celd 106 and celd 21 and 1.600 peak	esid 106 and seid 18 and 1.700 peak	esid 74 and esid 63 and 2.100 peak	esid 106 and esid 21 and 2.300 peak	esid 10s and esid 21 and 1.000 peek	eaid 74 and eaid 76 and 1.600 peak	resid 74 and resid 78 and 1.600 peak	esid 106 and esid 106 and 1.300 peak	esid 105 and esid 106 and 1.400 peak	esid 106 and esid 107 and 3.100 peak		resid 47 and ne resid 46 and ne 3.200 pesk 31
segid "BrD " and a segid "BrD " and a segid "BrD " and a sed	700	megid arb and 1.000	segid 'BrD ' and r segid 'BrD ' and r 2.500 1.600	egid BrD and r aegid BrD and r 2.600 1.700	aegid "BrD " and aegid "BrD " and 3.000 2.200	aegid 'BrD ' and r aegid 'BrD ' and r 2.500 2.100	megid "BrD " and r megid "BrD " and r 2.400 1.700	segid 'BrD ' and segid 'BrD ' and	segid BrD and	weid BrD and	segid 'BrD and r	2504 #91d BrD	segid BrD and segid BrD and 2.600 1.700	#914 BrD and r #914 BrD and r #914 BrD and r 2,900 2,100	6 2614) Begid "BED" and r C Begid "BrD" and r 1,200 2,600	segid BrD and segid BrD and 3.000 1.000	segid BrD and segid BrD and 2.500 1.600	70 • • nd 1.600	segid "BrD " and r segid "BrD " and r 2.300 1.300	agid 'BrD' and r aegid 'BrD' and r 2.400 1.400	eegid 'BrD and eegid 'BrD and 3.400 2.900	6.00.4 bn4 .00.4	segid srD snd
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4204				13		11.	and name HA2)	1 1 2		112				5.5	and name HB1 and name HG2	11:	100	11:	112				d name HAN) d name RA))		7
2.100 peek	resid 34 and 2	1.600 pear	2.000 peak resid 82 and	X.	resid 78 and 2.100 peak	resid 201 and resid 36 and 1.700 peak	reeld 201 ar	resid 201 and resid 30 and 1.700 peak	reeld 201 ar	resid 201 and resid 43 and 1.700 peak	resid 201 and resid 43 and 1.700 mak	resid 201 an	resid 201 an	resid 201 and resid 38 and 1.700 peak	resid 201 an	resid 201 and resid 43 and 1.700 peak	resid 201 an resid 43 an		resid 201 and n resid 38 and n 1.800 peak	resid 200 and resid 36 and	reeld 200 and	resid 200 and	11d 200 and 11d 38 and 1.700 pask	resid 200 and resid 43 and	1.800 peak
100	3 3	9	2.000 4nd re	2.700		M and res D and res 1.700	and res	1 - end res	end ree	2 2		2 2		and res	and res	1 * and res 1.700	and res	2 2	and res	1 and resid		u d	115 megid "AcH " and resid 200 megid "BrD " and resid 18 2.600 1.700 1.700 p		
, ,	(4264) eegid BrD .	2.500 1.600 (4304)	2.600 (4114) eegid BrD and	1300 3.	3.400 2.900		14 "Ack " and 14 "BrD " and 15	segid "AcH " and r segid "BrD " and 2 3.600 1.700	15} segid "Ack" and segid "big" and	_ * #	ų <u>.</u>	÷, i	45) segid "AcH " and segid "BrD " and	(eegid %ACH * and r segid "BrD * and r 2.600 1.700	ss) segid "AcH " and s	segid "AcH and segid BrD and 3.600 1.700	eegid Ack and eegid BrD and 2.700 1.800	A Act	I (95) [megid "Ach " and r megid "BrD " and r 2.700 1.800	{ 105} segid "Ack and segid "BrD and 2.600 1.700	_ F F	P. Ack	135) gid "AcH " gid "BrD "	ASSI (145) (segid "Ack " and re ((segid "BrD " and re 2,700 1.800	
3.8	A681 (43 1000)	A881 (+1		1. aegi 3.30 ASSI (43), eegi), eegi), eegi			-11.		-114			90 ((eegid 'h (megid 'h 2.600	200) 200)		(eegid (eegid 2.700	ABB1 { ((eegic (eegic (eegic 2.70	ASSI (109 (#egid (#egid 2.600	ASSI (115 (segid (segid (segid	ASSI (1) (engic) engic	ASBI (1) (megic ((megic 2,600	ABBI (14 (megic (megic	7.700
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	2.595	2.374			1.902	1.332		3.922	5.749	1.636	1.333	1.111	9			0.681	ייי.ר	3.667	1.885	1.496	1.701	1.088	4.017	7.924	
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	7.264 ppm2	7.266 ppm2	7.266 ppm2		7.266 ppm2	7.261 ppm2		7.069 ppm2	7.070 µpm2	7.070 ppm2	7.070 ppm2	7.069 ppm2	7.067 com2	. 63		7.017 ppm2	7.005 ppm2	7.005 ppm2	7.00 5 ppm 2	6.899 ppm2	6.686 ppm2	\$.740 ppm2	5.589 ppm2	5.577 ppm2	
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	E-03 ppm1	E+03 ppm)			faqq to.8	E+03 ppm		E.03 ppm1	E-03	E+03 ppm1	E+03 ppm3	8.02 ppm1	6.03 DOM			6.03 ppm.	E-03 ppm1	6.02 ppm1	K+03 ppm1	2+02 ppm1	8+03 ppm1	1+02 ppm1	1.02 ppm)	(+0) ppm;	
	0.12400E+03	0.109146+03	0.121865+03		0.13715E	0.13023E		0.15234E.03	0.15996E+03	0.207036+03	0.67243E+03	0.652318+02	0.200656+03	0.117486.03		0.254078.03	0.24279E.03	0.90985£+03	0.36097E+03	0.78199E+02	0.130808	0.75575E+02	0.787586+02	0.247618+03	
	volume	volume	volume		volume	volume		vol une	volume	volume	volume	volume	volume	volume		volume	volume	volume	volume	volume	volume	volume	volume	volume	
	0.10000E+01 volume	0.10000E+01	0.100008+01		0 . 10000E+61	0.10000E+01		0.10000E+01	0.100006.01	0.10000E+01	0.10000E+01	0.10000K+01	0.100006+01	0.100008+01			0.10000E+01	0.10000E+01	0.100008+01	0.10000E.01	0.10000E+01	0.10000E+01	0.100005.01	0.100005+01	
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Ame HDA	1224 weight	name HD4) name HB1)) 3234 weight	name KD) name KB)) 3254 weight		3264 weight name HD4)			3354 veight name HEN)		name KEt) name HB2)) 3404 weight	name HRV) name HD24) 3424 weight	name KE4) name KD4) 3444 weight	name HEt) name HD24) 3464 weight	name HZ)) name HD24) 3514 weight	name KZ }		3574 weight name MD4) name KE4)	3654 weight name HD!) name-HE!)	3684 weight name KDV) name HG2))	1754 weight	3804 weigh	1944 waight	4024 weight name KD2))		
p	103 and 1	4 2 5	* * * *	82 and n 103 and n	4	1 3	9 9 9	4 5	ē ×	2 5 ×	E E E		a but a	Para A	pur pur	* 45	7 - 4 - 4 - 4 - 4 - 4 - 4 - 4 - 4 - 4 -	1 2 3	A seed	Pack and and and and and and and and and and				A Para	
resid 82	12	25.	resid 82 resid 81 2.300	33,	. 45	-	9 9 9	7	2.200 peak	resid 102 2.100 per	117	resid 82 and resid 107 and 3.000 peak	resid 82 and regid 78 and r	reeld 82 and reeld 102 and r	resid 82 and resid 78 and	reeld 74	2.000 81d 74	2.200 mid 74	1.700 1.700 1.700	2.100 seid 46	2.400 14.46	22.100	: 8 :	8 3	
72	2.400	(segid BED and re (segid BED and re 3.200 2.600	* * * * * * * * * * * * * * * * * * *	pur		9 Pu		. 200 .	7 00 T	100 tr	and r	and r	* * * * * * * * * * * * * * * * * * *	• •nd •	p g	and r	2.800 2.000 [1654] segid BrD and r	700 and r		00	9	7. 00	į 11	0 g	•
ASSI { 3224}	14 - Bro	222	220		, 19 5 19 5 19 5 19 5 19 5 19 5 19 5 19 5	9-5	2 (P P P P P P P P P P P P P P P P P P	3	. (2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	2 g g 2	4 7 9 4 4 7 9 4	0.00		2 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	2 d d d	, de 1	2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		2 5 2 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5		1.400 (4024) 2.200 2.000 2.00	400 2 4054} 91d BrD	5	4
_ 1		9 9 7	6.6	- 6 6					20.7	555	2.40 2.40 2.40 4.24		100 m	1000	26) 35) 3 () 3	2 6 9	- 1 m	2 × 4 × 4 × 4 × 4 × 4 × 4 × 4 × 4 × 4 ×	2 6 6 6 6 6 6 6	9 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	2 2 2		405.	2 7 B	į

7.161 ppm2

0.48557£+03 ppm1

7.517

7.802 ppm2

0.100005+01

3.790

7.031 ppm2

0.96267E+02 ppm1

1.085

7.000 ppm2

0.78224E+02 ppm1

0.100005.01

1.08

1.029 ppm2

0.16527E.03 ppm1

0.723

4.026 ppm2

0.14933E.03 ppm1

1.609

4.023 ppm2

1.601

3.428 ppm2

ā

0.168316.03

0.11000E+01 volume

1.074

1.430 ppm2

ĕ

0.11000E+01

0.723

3.430 ppm2

0.14742E.03 ppml

0.11000E.01 volume

1.608

6.179 ppm2

0.11000E+01 volume

1.592

7.613 ppm.

0.13471E+03 ppm

0.11000E+01 volume

0.11000E+01 volume

0.11000E+01 volume

1.066

7.680 ppm2

0.691

7.690 ppm

0.727

2.547 ppm2

1.072

2.544 ppm2

0.29029E+03 ppm1

0.11000E+01 volume

1.603

2.536 ppm2

4.209

2.548 ppa2

0.173268+03 ppm

volume

2.547 ppm2 4.007 ppm3

3.

0.14313E+03 ppm1	
4 weight 0.11000E:01 volume 0.14313E:01 ppm1	
• weight	
1.800 peek	
1.800	
R (2.700	

7.481	7.483	7.63.7	, c	:	2	s								ę		•
ř			7.63.7	7.585	7.585	7.585	7.350		7.358	7.35	7.358	7.350		7.350		7.358
4.015 ppm2	3.429 ppm2	4.015 ppm2	3.429 ppm2	4.015 ppm2	3.429 ppm2	3.542 ppm2	4.019 ppm2		3.430 ppm2	3.430 ppm2	1.430 ppm2	3.430 ppm2		3.430 ppm2		3.430 ppm2
0.139248+03 ppm1	0.152298+03 ppm1	0.18465E+03 ppml	0.13938E+03 ppm1	0.16075E+03 ppml	0.162918+03 ppm1	D.140498+03 ppm1	0.16796R+03 ppm1		o.ierelktol ppmi	0.120008+03 ppm1	0.120008+03 ppm1	0.12000K+03 ppm1		0.120008+03 ppm1		land consecution
0.110006+61 volume	0.11000E+01 volume	0.110008+01 volume	0.11000E+01 valume	0.11000\$+01 volume	0.11000E-d1 volume	0.11000E+01 volume	0.11000E-01 volume			0.11000E+01 volume	0.11000E+01 volume	0.11000&+01 volume		0.11000E+01 volume		
magid *AcM: and resid 101 and name NA2)	eegid Act and resid 201 and name HB1)] segid Err and resid St and hame HB1) 1.00 1.700 pask 26 wight 25] segid Act and resid 201 and name HB2)] segid TEP and resid 33 and name HB2)	segid "Acid and resid 201 and name MA1)) segid "BrD and resid 80 and name MD1) 315 segid Acid and resid 20 and name MA2)) segid Acid and resid 201 and name MD1) segid "BrD" and resid 201 and name MD1)	10.04 Acti - and resid 201 and name HB2) segid "Acti - and resid 84 and name HB2) 42 1.400 1.400 peak 44 weight segid "Acti - and resid 201 and name HB2) segid "BCD - and resid 201 and name HB2)	aegid "AcH" and reaid 301 and name [AZ]) segid "BrD" and reaid 35 and name [ER] 56] 1.700 1.700 segid "AcH" and reaid 31 and name [AZ] segid "AcH" and reaid 31 and name [AZ])	### *** Act ** and resid 201 and name HB1)) ###################################	megid "AcH" and resid 200 and name NAN) eegid "BrD" and resid 95 and name HEN] 2.700 1.800 1.800 peak 76 weight	regid "AcH" and resid 301 and name HA1)) segid "AcH" and resid 88 and name HR1) 2.60 11.700 11.700 peak 66 weight accid "Ach" and accid "Ach" ac	**************************************	segid AcH and resid 201 and name HB1)) segid *BrD and resid &s and name HEv)	eegid "AcH " and resid 200 and name MAN) eegid "AcH " and resid 201 and name HN)) 2.00 1.800 1.800 peak 7 weight 1.71	megid "AcH " and resid 200 and name HAN) segid "AcH " and resid 201 and name HAN)) 2.700 1.800 1.800 peak 17 weight (27)	Begid 'AcH - and resid 201 and name HB2)) Begid 'AcH - and resid 201 and name HD1)) 2.700 1.800 1.800 peak 27 weight 27)	eegid "AcH * and resid 201 and name eegid "AcH * and resid 201 and name [17]	### ### ### ### ### ### ### ### ### ##	wegold "Acci " and resid 201 and name HB2)) seepid "Acci " and resid 201 and came HB1)) equal "Acci " and resid 201 and came HB1)) equal "Acci " and resid 201 and name HB2)) 2.700 Acci " and resid 201 and name HB2)) 2.700 Acci " and resid 201 and name HB2))	eegid "AcM " and resid 201 and name Mai)) eegid "AcM " and resid 201 and name HM))
ASS	3 - 73 - 184 00 - 184	5 5	# 5 F	# 0 F	1984	7	= =====================================	189V .)) j	4)))	35 g	Yes	33 -: 8	79 Y 20 Y 2	5 5

Ambiguous NOE-derived Inter-proton Distance Restraints

1.410	1.774	1.61	3,726	2.497	2.294	. 518.
1.738 ppm2	9.740 ppm2	0.673 ppm2	7.977 ppec	8.612 ppm2	9.107 ppm2	6.544 ppm2
0.35326E+02 ppm1	0.204178.03 ppm1	0.45845K+02 ppm1	+03 ppm1	+02 ppm1	. O. pps. 1	tudd to
			cne 0.176458.03 ppm.1	me 0.120218+02 ppm1	ne 0.61178E+01 ppm1	o 0.136088403 ppm1
0.10000£-01 volums	0.10000&+01 volume	0.10000E+01 volume	0.10008*01 volume	0.10000E+01 volume	0.10000K+01 volume	0.10000E.01 volume
MO)) Weight Weight HM)) HM))	H H H H H H H H H H H H H H H H H H H	HB2)) HB2)) HB2)) HB2))	Meight () () () () () () () () () () () () ()	HN 1) HB1 1) HB2 1) HB2 1) Weight HR 1)	HN)) weight HN)) HD1)) HB1))	HR))
and name and	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	T to the state of	Σ.	and the same	and name and name and name and name and name	and name and name peak 1551 and name
and resid 32 4.200 p. 300 p. 3			and resid 97 2.300 2.300 and resid 78 and resid 79 and resid 95 and resid 96		and resid 16 00 0.000 and resid 75 and resid 72 and resid 98 and resid 98	and resid 21 and 22 and 23 and resid 24 and resid 106 and resid 26 and resid 25 and resid 25 and resid 22 and resid 23 and resid 23 and resid 24
()11) 600.4 861 1.10	1931 190	781 804 6954 805 805 805 805 805 805 805 805 805 805	9.100 3.600 9.000 9.100	9914 '980' and resid 25 (110) and resid 37 (110) and resid 78 (1102) and resid 60 (110) and resid 60 (eegid 'BID' and 3.300 5.300 1101) eegid 'BID' and segid 'BID' and 1101) eegid 'BID' and eegid 'BID' and	1851 9.00 and 4.00 and 3.400 and 3.400 and 3.400 and 3.400 and 4.000 and 4.0
ASSI OR ((A4551	ob See	5 5 5 5	A681 C.		

3.631	2.954	2.8	**	•	2 . 969	2.5	3.204
5.196 ppm2	6.734 ppm3	6.809 ppm2	8.810 ppm2	9.156 ppm2	6.661 ppm2	* 133 pps3	6.166 ppm2
0.12549E.03 ppm.1	0.41938E+02 ppm1	0.402026.02 ppm1	0.672416+02 ppm1	0.56619E+03 ppm1	0.248218+02 ppm1	0.59139E+02 ppm.	0.16212E+03 ppm1
E 0.10000E.01 volume	0.10000E.01 volume	0.10000E.01 volume	0.10000£+01 volume	0.10000E+01 volume	0.100005.01 volume	0.10000E+01 volume	0.10000E.01 volume
peak 1781 weight and name HH)) and name HB)) and name HB2)) peak 2721 weight and name HB2)) and name HB2))	and name HB2 and name KB2 and name KB2 peak 1261 weig and name HB3 and name HB3	and name HU)) pack 1361 weight and name HU)) and name HU)) and name HU)) pack 1311 weight and name HU)) and name HU)) and name HU)) and name HU))	and name HN)) and name HD1)) peak 3401 weight and name HN)) and name HO1)) and name HO1))	and name HN and name HB1 and name HB1 and name HB	Dame Hill Dame H	A 10 10 10 10 10 10 10 10 10 10 10 10 10	6751 6751 6751 Pame
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			2.49	1.72	2.56	2.316		2.150	2.002	3.908	2.352
9914 170			8.573 ppm2	8.574 ppm2	9.740 ppm2			9.742 ppm2	9.740 ppm2	9.464 ppm2	9.463 ppm2
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9.462 ppm2

4.678

9.472 ppm2

7.510

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3.066

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2.13

8.557 ppm2

3.108

8.556 ppm3

2.851

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1.929

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	volume							l volume 0.5			volume 0.6
0.10000£.01 volume	0 . 10000K+01	0.10000g.ol volume	0.10000E+01 volume	6.10000E.01 volume	0.1000GR+01 volume		6.10000E+01 volume			0.10000E+01 volume	
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3. 661	4.947	1.460	1.920	3.626	3.146	3.659		2.943	3.284	1.973	2.115
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8.306 ppm2	6.039 ppm2	8.045 ppm2	9.125 ppm2	9.135 ppm2	6.669 ppm2	8.669 ppm2
0.133266.03 ppn.1	0.36902K+02 ppm1	0.826828.02 ppm1	0.64847E+02 ppm3	0.66527E+02 ppm.1	0.578276+02 pm.1	0.26537E+04 ppm1
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and name HH))	and name	and name HN)) park lists weight and name HN)) and name HN)) and name HN))	and name	and name HM) peak 12011 weight and name HB)	and the and mass NA)) and 100 and mass NA)) aid 20 and mass NA)) aid 100 and mass NA)) aid 30 and mass NA)) aid 30 and mass NA)	and name HN)) ak 12101 weight and name HN))
	resid 70 1.300 1.5	resid 73 resid 73 resid 73 resid 23 resid 23	OR (11931) (1 segid "PPP" and resid 75 (1 segid "PPP" and resid 75 (1 segid "PPP" and resid 75 (1 segid "PPP" and resid 100 (1 1391) (2 segid "PPP" and resid 100 (1 1391) (3 segid "PPP" and resid 100 (1 1391) (4 segid "PPP" and resid 100 (1 1391) (5 segid "PPP" and resid 31 (1 1391)	(eagid 'BrD' and reaid 23 (eagid 'BrD' and reaid 22 1.00 1.7	The and resident to an analysis and resident to an	one and one of
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8.218 ppm2

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4.568 ppm2	8.545 ppm2	9.463 ppm2	9.473 ppm2	ppm2	7.762 pped	4.695 ppm2	9.156 ppm2
0.17809E.03 ppm1	0.41104E+02 pps1	0.44090E-02 ppm1	0.68908B.02 ppm1	0.144556.02 ppm1	0.306798:02 ppml	0.92105£+02 ppm1	0.494066.03 ppm1
• • • • • • • • • • • • • • • • • • •	0.10000£-01 volume	0.1000E-01 volume	0.10000£.01 volume	0.100006.01 volume 0.10000E.01 volume	0.100005.01 volume	0.1000E+01 volume	0.10000E-01 volume
and name HW)) and name HB2)) and name HV2)) and name HD2) and name HD1) and name HD1) peak 13191 weight	and name HN1) and name HO1) and name HO2) and name HO2) and name HO30 beat 13201 weight	and name	and name and name and name and name	and name NG2 and name HN and name HN and name HG4	and name and	and name and	11.500 peak 14151 weight. 141 02 and name HHz)) 141 02 and name HHz)) 141 102 and name HHz)) 151 102 and name HHz)) 151 103 and name HHz) 151 103 and name HHz) 151 103 and name HHz)
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8.147 ppm3	9.120 ppm2	9.119 ppm2	9.119 ppm2	9.119 ppm2	9.196 ppm2	8.544 ppm2	6.365 ppm2
0.41415E+02 ppm1	0.234528+03	0.5052E402 ppm1	0.12055R+03 ppm1	0.54095E+02 ppm.)	0.10060E+03 ppm1	0.10298E+03 ppm1	0.61364E+03 ppm1
0.10080E+01 volume		0.10000E+01 volume	0.10000E+01 volume		0.100008+01 volume 0.100008+01 volume	0.10000E.01 volume	0.10000K+01 volume
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0.330978+02 ppm1

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1.961

8.568 ppm2

0.10000£+01 volume

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resid 62 2.000 p resid 62 resid 62

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8.570 ppm2

0.24650E+02 ppm1

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9.035 ppm2

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9.037 ppm2

volume 0.46525E+02 ppm1

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peak 14461 weight

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0.46826E-02 ppml	0.214248+03 ppm1	0.14748E.02 ppm1	0.16152E+03 ppm1	0.24679E-03 ppm1	0.34635K+03 ppm1	0.59623E+03 ppm1	0.20695R+03 ppm1	0.97985E+02 ppm1	0.37938E-02 ppm3	0.29812E+02 ppm1	0.812698+02 ppm1	0.21510E+03 ppm1
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0.58075E+02 ppm1	0.54622E+02 ppm1	0.20227E+03 ppm1	0.30480E.02 ppm.1	0.64483E+02 ppm1	0.30\$51£*03 ppm1	0.92898-01 ppm1	0.31671E.02 ppm1	0.600765.02 pml	0.34186E.02 pm.	0.27108E+02 ppm1	0.22158E-02 ppm1
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4.564	1.428	2.14	1,223	**	2.352	3 . 320	1. 997	er.	1.710
1.554 ppm2	1.995 ppm2	4.853 ppm2	4.83 ppm2	1.747 ppm2	3.747 ppm2	4.656 ppm2	2.832 ppm2	4.656 ppa2	4.656 ppm2
0.2957&K+02 ppml	0.21357E+03 ppm1	0.545646+02 ppm.l	0.12632E-02 ppm1	0.691046+03 ppm1	0.34685E+03 ppm)	0.47335E+03 ppm1	0.871778+02 ppm1	0.359408.03 ppml	0.56651E.03 ppm1
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4.459 ppm2	3.90 ppm2	1.786 ppm2	4.163 ppm2	1.056 ppm2	1.056 ppm2
0.413448.02 pps.1	0.13575E+01 ppm1	0.235326.03 ppm1	0.17412E-02 ppm1 *	0.780596.02 ppm.1	0.25206K-02 ppm1
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0.100008+01 volume 0.583118+02 ppm1	ē	+03 ppm1	Ppm1 1.650	0.33144E-03 ppm1 1.648	ppa1 1.649
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and resid 111 and name (M.)) and resid 110 and name (M.)) and resid 24 and name (M.)) 700 3.200 peak 20672 weight 0.100008-01 volume and resid 21 and name (M.)) and resid 32 and name (M.)) and resid 32 and name (M.)) and resid 41 and name (M.)) and resid 61 and name (M.)) and resid 62 and name (M.)) and resid 62 and name (M.))	Test d 35 and hame M 1) Test d 55 and hame M 1) Test d 61 and hame M 1) Test d 62 and hame M 1)	id 73 and name HD11) 14 25 and name HC21) 2.400 peak 2072 weight 0.10000E-01 volume 0.98567E-02 ppm1 14 25 and name HC21) 14 106 and name HC21) 14 14 And name HC21)	9EP - and resid 35 and name HR1) 3.700 2.300 peak 20832 weight 0.10000&01 volume 0.603718.02 ppm1 1.650 8EP - and resid 58 and name HD2) 8EP - and resid 58 and name HD2) 8EP - and resid 58 and name HD2) 8EP - and resid 12 and name HD3) 8EP - and resid 102 and name HD3) 8EP - and resid 102 and name HD3) 8EP - and resid 30 peak 20842 weight 0.10000&01 volume 0.150618.02 ppm1 1.649 8EP - and resid 58 and name HD3) 8EP - and resid 58 and name HD3)	"BITD - and resid 58 and mass HGI\$) "BITD - and resid 61 and mass HGI\$) "BITD - and resid 61 and mass HGI\$) "BITD - and resid 51 and mass HGI\$) "BITD - and resid 52 and mass HGI\$) "BITD - and resid 53 and mass HGI\$) "BITD - and resid 55 and mass HGI\$) "BITD - and resid 56 and mass HGI\$)	Traid 51 and name HB2 1) Traid 55 and name HD21) Traid 32 and name HD21) Traid 32 and name HD21) Traid 32 and name HD21) 1.600 peak 21112 weight 0.100006.01 volume 0.120598.02 ppml 1.649 Traid 32 and name HB2 1) Traid 32 and name HB 1) Traid 42 and name HB 1) Traid 43 and name HB 1)

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8.120	1.417	4.256	•	4.939	4.637	1:003	4.574	•	7.534	4.61	3
2.615 ppm2	2.615 ppm2	4.952 ppm2	4.952 ppm2	5.477 ppm2	5.297 ppm2	4.656 ppm2	1.400 ppm2	1.401 ppm3	3.866 ppm2	3.867 ppm2	3.667 ppm2
0.93859£+02 ppm1	0.10852E.03 ppm1	0.24494E+01 ppm1	0.72079£+02 ppm1	0.538868.02 ppm1	o.1381Esca ppm	0.67221E+02 ppm1	0.36871E+03 ppm1	0.23#318*02 ppm1	0.13082E+03 ppm1	0.133278+03 ppm1	.360148.03 ppm)
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neme MG2)) neme MA)) (3212 weight 0. neme MG1))	1 name NO1) 23252 weight 1 name NO1) 1 name NO1)	name HA)) (3382 waight name HA)) name HA))	name HA 1) name HA 1) (3392 weight name HA 1) name HA 1)	name NA 1) name NA 1) 19512 waight name NA 1) name NA 1)	name KA)) 1352 weight 1352 weight name KA)) name KB))	name HA 1) name HA 1) name HB14) 1562 weight name HA 1) name HG14)	Name KD24) Name NA)) 13772 weight name KO1)) Name KA))	name MD34) name MA 1) 3792 waight name MO1))	name HA 1) name HEA) 13672 weight name HA)) name HDA)	I name KA 1) 23692 weight name KA)	Annual MA () () () () () () () () () () () () ()
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1.433	1.415	1.596	1.177	1.986	3.650	3.471	3.414	4.516	2.383	4.67
2.140 ppm2	0.911 ppm2	0.415 ppm2	0.416 ppm2	0.415 _. ppm2	0.416 ppez	1.649 ppm2	1.649 ppm2	1.649 ppm2	4.310 ppm2	4.310 ppm2
0.53948E+02 ppm1	0.16641E+02 ppm1	0 .18200E+00 ppm1	0.15952E+03 ppm.1	0.21517E+02 ppm1	0.23228+03 ppm1	0.15293E-03 ppm1	0.106146:03 ppm1	0.45951E+02 ppm1	0.10572E+03 ppm1	. 0.312558.03 ppm1
0.10000K+01 volume	0.10000E+01 volume	0.10000E+01 volume	0.10000E.01 volume	0.10000E.01 volume	d.10000E.01 volume	0.10000E+01 volume	0.1000E+01 volume	0.10000E.01 Volume 0.45951E.02 ppm1	0.10000£+01 volume	0.100008:01 volume 0.31255E.02 ppm1
and name HD2%) peak 23912 weight and name HB1 }} and name HG2%)	and name HD21) and name HD21) peak 23942 weight and name HB2)) and name HB2)	and neme HD24) and name HO24) peak 24102 weight and name HD24) and name HD24)	reid 16 and name HD24) 2.000 peak 24112 weight sid 18 and name HD24) sid 14 and name HD24)	14d 10 and name HD21) 14d 14 and name HD21) 14d 15 and name HD21) 14d 11 and name HS1) 1.600 peak 24122 weight 14d 16 and name HS1)	and name peak 24292 and name	and name HD2%) and name HB2)) and name HB1) pusk 24492 weight and name HB1) and name HB2))	And name HD19) peak 24501 weight and name HD19) and name HB1) And name HB1)	peak 24532 weight and name HD14) and name HD24) and name HD24) and name HB24) and name HB1)) seak 24602 weight	and name KB2)) and name KA)) and name KA)) peak 24692 weight and name KA)) and name KB)	and name HA !) and came HA !) peak 34712 weight and name HA !) and name HA !) and name HA !)
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(segid 3.400 OR (23912) ((segid (segid AASS (23954	(megid (megid (100 OR (21942) (megid (megid (megid	08 (24102) (***)	ASSI (24113) (2-200 OR (24113) (24113) (24113) (24113)	A851 (24123) A851 (24123) (26914) (26914) (26914) (26914) (26914) (26914)	A581 (24292) (megid '(megid ')) 1000 OR (24292) (megid ')	ASSI (2442) (aegid (aegid (aegid (ASSI (2450) (eegid (eegid (eegid (eegid (eegid (eegid (eegid	1.500 OR (24512) (megid (eegid ABSI (24602) (megid (megid (megid (megid (megid (megid (megid (megid	A881 (26692) ((eegid "(eegid ") 000 0R (24692) ((eegid ") (eegid ")	

(1) (1)	4.574		4.61						3	•				.63		;		100			;	•			4.907	
### ### ### ### ### ### ### ### ### ##	1.969 ppm2		1.969 ppm2		1.495 ppm2	•			2.190 ppm2	1.57		4.358 8082	!	4.360 ppm2		1.644 poss		1.648							1.20% ppm2	
#### #### ############################	0.24704E-03 ppm1		0.281618-02 ppm1			:			o.resisting part	0.10950E+04 pcm1		0.387948+02 ppm1		.128065.04		0.405586+03 ppm1		0.24225E+02 ppm1	:		0.24691E-01 pms1				rudd to manner of	
1.700 pask 3.733 weight 1.400 pask 3.733 weig	00E+01 volume		00E-01 volume		ODE+01 volume									5		volume		volume			volume			<u> </u>		
1.100 past 2.000 past		NB2 1) NB1 1)		KB1))		K01 11							2 - 1 6		191		(1012)) (82))		(10)	(123)) (124)	•		(10 (1)			500
### ### ### ### #### #################	and name ond name	and name	and name and name peak 24732	and name	and name and name peak 24772	and name	and name	and name and name	and name	and name and name poak 24852	and name	and name and name	and name	and name and name peak 24992	and hame	and name and name peak 25052	and name and name	and name and name peek 25113	and name	and name	and name and name	and name	and name and name	and name and name peak 25162	and name	and name
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7	11		- 2 2	2 2	2.2	2 2	11	11"	11		11	2 2	11	2 2	2 2	1		resid 21	r e e	100	1		resid 21		2 2	2 2
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), 100 ((eegid (), 100	(segid BrD and r ((segid BrD and r 3.100 2.400	2.400	resid 110 and name resid 114 and name 2.400 peak 25562		ind nam	# HA2))	0.10000E+61 volume	01 volume	0.901316.02	4	1.28	4 ppm2	4.509	
	114 .Bri	bus.	resid 110	95	and name	H026)						;		
	(segid 'BrD ' and r ((segid 'BrD ' and r 2.800 2.000	2.000	resid 110 and name resid 14 and name 2.000 peak 25872	318	ind new ind new ik 2587	HDIV)	0.10000E+01 volume	01 volume	0.152566.03 ppm1	ã	1.15	1.154 post	***	
	OR (25872) (eegid "BrD " and ro (eegid "BrD " and ro	pue .	resid 110	2:	and name	HOLV SA			!	į				
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	, p. p.	pue .	resid 110 resid 116	23	and head	HG2V1								
	(segid BFD sand r (segid BFD sand r 1.100 2.400	2. 60 E	resid 110 resid 17 2.400 p	222	seld 110 and name seld 17 and name 2.400 peak 25693	ME KD14)	0.10000E+01 volume	Di volume	0.95482E+02 ppm1	į	1.15	1.154 ppm2	4.834	ţ
	14 Brt	bus.	resid 110		aman bna	101						:		
9 9 9	(segid 'BrD " and re ((segid 'BrD " and re 3.000 3.200	2.200	reald 110 and name reald 106 and name 2.200 peak 25902 a	200	nd nam nd nam k 2590;	HD3N) HA))	0.10000K+01 Volume	01 volume	0.11502E+03 ppm1	ī wada	1.15	1.154 ppm2	4.568	
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0.00	7 7 8 8	2.600	resid 1 resid 1 2.30		nd new nd new k 2602;	- HD14) - HB2)) 2 veight	0.10000E+01 Volume	ll volume	0.704308+02	1800	1.15	i di	636	
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0.51512E.01 ppm1	0.33282E+02 ppm1	0.18876E+02 ppm1	0.303716.02 ppm1	0.10851E+04 ppm1	0.208256.02 ppm1	0.208306.03 pps1	0.44195E+03 ppm1	0.61541E-02 ppm1	0.92579K•02 ppm1	0.43704E+02 ppm1	0.521405+02 ppm.
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	7.907 ppm2	7.904 ppm2	7.888 ppm2	7.900 ppm2	7.896 ppm2	7.893 ppma	7.891 ppm2	7.691 ppm2	7.888 ppm2	7.889 ppm2
	0.10000E.01 volume 0.61601E.03 ppml	0.10000E+01 volume 0.15243E+04 ppml	0 54441E+03 ppml	0.60159E+02 ppml	0.12306E+03 ppm1	0.47618E-03 ppm1	0.54491E-03 ppml	0.3083E-03 ppm1	0.84175£+02 ppml	0.45504E+03 ppm1
		0.10000E+01 volume	0.10000E+D1 volume	0.10000E+01 volume	0.100006+01 volume 0.123066+03 ppm1	0.100006+01 volume 0.47618E+03 pps1	0.10000E+01 volume	0.10000E+01 volume 0.10081E+01 ppm1	0.10000E+01 volume	0.10000E+01 volume 0.45504E+01 ppm1
73	14 and name K2) 19 and name HB% 10 peak 1104 weight 14 and name K2) 13 and name HD2)	id 68 and name HBt) id 68 and name HDt) 1.100 peak 1114 weight id 107 and name HBt) id 107 and name HBt)	and name and name and name peak 1124	said 68 and name HEY) said 68 and name HEY) 1.900 peak 1134 weight 1.900 peak 1134 weight 1.81d 68 and name HEY) said 73 and name HCY)	and name HE') peak life weight and name HE') and name HE')	16 and name HER) 6 and name HER) 6 and name HER) 6 pask 1204 weight 7 and name HER)	4 and name H2 1) 2 and name H2 1) 07 and name H2 1) 9 peak 1344 wight and name H2 1) 6 and name H2 1)	and 107 and name HEN) 1.800 peak 1254 weight sid 68 and name HEN) sid 59 and name HEN)	and name and name and name and name and name	peak 1364
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	0.10144E.03 ppm1		0.38056R+03 ppm1		0.19434E.03 ppm1					Tudd course	0.27794£+03 pom3			0.11624K+04 pres			0.46212E+03 ppm1		0.27340E+03 ppm1			208108-03 prest		0.23703£+03 pgm1	:		
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et piest pe . c	1	3 8	Ē	and resid 78	"BrD " and resid 74 "BrD " and resid 22	1.400 1.400 pmak	o and resid 106		"BrD" and resid 96	2.400 3.400 peak	and resid	and resid 15	3	• and resid 64	"BrD " and, resid 15	and resid 11	BrD and resid 34	end reeld 32	and resid se	2.400 2.400 peak	and bloom but a	BrD and resid 33	ond resid 96	and res	2.700 2.200 peak	"BrD " and resid 106	PG.		•	end resid 115	BrD and resid 106	CIT DIMA DUE	BrD and resid 106	3.400 2.400 peak	and resid 96	and resid 86	and resid 74	2.200 2.200 peak	- 1	BrD and resid 109		and resid 28	2.400 2.400 peak	and resid 68	BrD and resid 54	and resid 106		2.100 2.100 peak	and resid 74
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Table 4

Hydrogen Bonding Restraints

!Helix Z assign (residue 19 a assign (residue 19 a		(residue 15 and name O) (residue 15 and name O)	1.80 0.0 0.40 2.80 0.30 0.40
assign (residue 22 a assign (residue 22 a			1.80 0.0 0.40 2.80 0.30 0.40
assign (residue 23 a assign (residue 23 a		(residue 19 and name O) (residue 19 and name O)	1.80 0.0 0.40 2.80 0.30 0.40
assign (residue 24 a assign (residue 24 a	nd name HN)	(residue 20 and name O) (residue 20 and name O)	1.80 0.0 0.40 2.80 0.30 0.40
assign (residue 25 a	nd name HN)	(residue 21 and name O)	1.80 0.0 0.40
assign (residue 25 a	nd name N)	(residue 21 and name O)	2.80 0.30 0.40
!Helix B assign (residue 75 a assign (residue 75 a		(residue 71 and name 0) (residue 71 and name 0)	1.80 0.0 0.40 2.80 0.30 0.40
!assign (residue 77 :) (residue 73 and name O)) (residue 73 and name O)	1.80 0.0 0.40 2.80 0.30 0.40
assign (residue 78 amassign (residue 78 am		(residue 74 and name 0) (residue 74 and name 0)	1.80 0.0 0.40 2.80 0.30 0.40
assign (residue 79 amassign (residue 79 am		(residue 75 and name 0) (residue 75 and name 0)	1.80 0.0 0.40 2.80 0.30 0.40
!assign (residue 80 a) (residue 76 and name 0)) (residue 76 and name 0)	1.80 0.0 0.40 2.80 0.30 0.40
assign (residue 81 amassign (residue 81 am		(residue 77 and name 0) (residue 77 and name 0)	1.80 0.0 0.40 2.80 0.30 0.40
assign (residue 82 amassign (residue 82 am		(residue 78 and name 0) (residue 78 and name 0)	1.80 0.0 0.40 2.80 0.30 0.40
!Helix C assign (residue 102 a	and name HN) (residue 98 and name O)	1.80 0.0 0.40
assign (residue 102 a) (residue 98 and name O)) (residue 99 and name O)	2.80 0.30 0.40 1.80 0.0 0.40
assign (residue 103 a	and name N	(residue 99 and name O)	2.80 0.30 0.40
assign (residue 104 a assign (residue 104 a) (residue 100 and name O)) (residue 100 and name O)	1.80 0.0 0.40 2.80 0.30 0.40
assign (residue 105 a assign (residue 105 a) (residue 101 and name O)) (residue 101 and name O)	1.80 0.0 0.40 2.80 0.30 0.40

ATOM 64 NB LVS 6 23.736 3.06 -6.238 1.00 ATOM 65 NB LVS 6 23.532 3.630 -6.238 1.00 ATOM 75 NB LVS 6 23.837 2.600 -6.238 1.00 ATOM 71 CB LVS 6 23.647 27.40 1.00 ATOM 71 CB LVS 6 22.669 1.413 -6.409 1.00 ATOM 71 HIS LVS 6 22.669 1.403 -6.409 1.00	74 CG LYYS 6 72.00 1.000	ATOM 60 CE LVS 6 23.2470 0.004 -9.788 1 ATOM 60 CE LVS 6 21.669 -0.104 -0.514 1 ATOM 61 HE1 LVS 6 21.107 -0.129 -7.608 1 ATOM 62 HE2 LVS 6 20.987 -0.509 -7.508 1 ATOM 63 HE2 LVS 6 20.987 -0.509 -9.727 3	ATOM 64 H21 LVS 6 23.330 1.081 9.014 1 ATOM 65 H22 LVS 6 21.330 1.081 6.014 1 ATOM 66 H22 LVS 6 23.848 1 4.35 1.35 1.35 1.35 1.35 1.35 1.35 1.35 1	ATOM 87 C LYS 6 20,776 2.397 -8,446 1 ATOM 88 0 LYS 6 20,863 1,638 -4,471 h	ATOM 89 H GLU 7 19-646 3.031 -5.773 1 ATOM 90 HH GLU 7 19-637 3.606 -6.552 1	92 HA GLU 7 18.531 1.926 -4.418 1	94 HB1 GLU 7 16.500 4.011 -4.064 1	95 CG GLM 7 10.875 1.904 -2.761 1	## HOS OLU 7 19:744 3.154 -3.676 1	29 CD GLU 7 18:025 3:516 -1:519 1	101 OK2 GLU 7 18.383 2.483 -0.947 1 102 C GLU 7 17.215 2.662 -5.928 1	103 O GLU 7 16.278 3.461 -5.886 1 104 N PRO 8 17.218 1.617 -6.772 1	105 CA PRO 8 16.120 1.352 -7,702 1 106 NA PRO 8 15.785 2.256 -8.189 1	ATOM 107 C9 PRO 6 16.760 0.419 -6.727 1 ATOM 106 HB1 PRO 6 17.200 1.002 -9.523 1	109 HB2 PRO 8 16.011 -0.245 -9.130 1 110 CG PRO 8 17.796 -0.327 -7.958 1	111 HU1 PMU B 17.357 -1.205 -7.508 1 112 HU2 PMO B 18.607 -0.608 -8.614 1	113 CD PMO 6 16,294 0,613 -6,889 1 114 MD1 PMO 6 18,429 0,065 -5,996 1.	115 HD2 PRO 8 19.230 1.076 -7.197 1.	117 U PRO 6 13.762 0.924 -7.360 1. 118 N ARG 9 15.236 -0.196 -6.057 1.	120 CA ARG 9 14.139 -0.917 -5.328 1.121 KA ARG 9 13.522 -0.189 -4.906 1.	122 CB ABG 9 13.421 -1.630 -6.279 1.	124 HB2 ARG 9 12.776 -1.222 -6.898 1. 125 CG ARG 9 14.313 -2.661 -7.188 1.	126 HQ1 ARG 9 14.295 -2.236 -8.181 1.	128 CD ARG 9 13.843 -4.106 -7.262 1. 129 HD1 ARG 9 13.631 -4.106 -7.262 1.	130 HD2 ARG 9 12.644 -4.125 -7.671 1	132 HE ARG 9 15.302 -4.464 -6.735 1	134 NH AND 9 13,960 -6,908 -7,208 1,	135 MH12 AND 9 13:342 -6.401 -6.606 1.	137 NH2 ANG 9 15.563 -6.932 -6.850 1. 138 HH21 ANG 9 16.157 -6.444 -9.489 1.	139 HH22 ARG 9 15,565 -7,931 -6,810 1.	141 O ARG 9 14,421 -2,897 -3,991 1, 142 N ASP 10 15,732 -1,144 -3,456 1,	143 HN ASP 10 15.988 -0.223 -3.673 1.	145 HA ASP 10 17.067 -2.540 -2.760 1.146 CB ASP 10 17.169 -0.613 -1.457 1.	147 HB1 ASP 10 17,594 -0.061 -1.1497 1.146 HB2 ASP 10 16,490 -0.141 -0.602 1.	149 CG ASP 10 16.292 -1.457 -0.706 1.	151 OD2 ASP 10 18-692 0.886 0.329 1.	151 C ASP 10 15,383 -2,565 -1,466 1.	154 N PRO 11 15,249 -3.689 -1.658 1. 155 CA PRO 11 14,309 4,709 -0.867 1.	156 MA PRO 11 13,311 -0,257 -0,920 1.	15e HB1 PRO 11 13,211 -6,399 -1,772 1.	159 HB2 PRO 11 14,849 -6,791 -0,999 1. 160 CO PRO 11 15,036 -5,829 -2 888 1
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1.144 1.00 0.00 BFD ATCH 103 IEL LYS 6 1.144 1.00 0.00 BFD ATCH 104 IEL LYS 6 1.232 1.00 0.00 BFD ATCH 104 IEL LYS 6 1.245 1.00 0.00 BFD ATCH 104 IEL LYS 6 1.245 1.00 0.00 BFD ATCH 104 IEL LYS 6 1.245 1.00 0.00 BFD ATCH 104 IEL LYS 6 1.245 1.00 0.00 BFD ATCH 104 IEL LYS 6 1.245 1.00 0.00 BFD ATCH 104 IEL LYS 6 1.245 1.00 0.00 BFD ATCH 110 O. LYS 7 1.245 1.00 0.00 BFD ATCH 111 O. LYS 7 1.245 1.00 0.00 BFD ATCH 112 IEL MILL LYS 6 1.245 1.00 0.00 BFD ATCH 113 IEL MILL LYS 6 1.245 1.00 0.00 BFD ATCH 113 IEL MILL LYS 6 1.245 1.00 0.00 BFD ATCH 113 IEL MILL LYS 6 1.245 1.00 0.00 BFD ATCH 113 IEL MILL LYS 6 1.245 1.00 0.00 BFD ATCH 113 IEL MILL LYS 6 1.245 1.00 0.00 BFD ATCH 113 IEL MILL LYS 7 1.245 1.00 0.00 BFD ATCH 113 IEL MILL LYS 7 1.245 1.00 0.00 BFD ATCH 113 IEL MILL LYS 7 1.245 1.00 0.00 BFD ATCH 113 IEL MILL LYS 7 1.245 1.00 0.00 BFD ATCH 113 IEL MILL LYS 7 1.245 1.00 0.00 BFD ATCH 113 IEL MILL LYS 7 1.245 1.00 0.00 BFD ATCH 113 IEL MILL LYS 7 1.245 1.00 0.00 BFD ATCH 113 IEL MILL LYS 7 1.245 1.00 0.00 BFD ATCH 113 IEL MILL LYS 7 1.245 1.00 0.00 BFD ATCH 113 IEL MILL LYS 7 1.245 1.00 0.00 BFD ATCH 113 IEL MILL LYS 7 1.245 1.00 0.00 BFD ATCH 113 IEL MILL LYS 7 1.245 1.00 0.00 BFD ATCH 113 IEL MILL LYS 7 1.245 1.00 0.00 BFD ATCH 113 IEL MILL LYS 7 1.245 1.00 0.00 BFD ATCH 113 IEL MILL LYS 7 1.245 1.00 0.00 BFD ATCH 113 IEL MILL LYS 7 1.245 1.00 0.00 BFD ATCH 113 IEL MILL LYS 7 1.245 1.00 0.00 BFD ATCH 113 IEL MILL LYS 7 1.245 1.00 0.00 BFD ATCH 113 IEL MILL LYS 7 1.245 1.00 0.00 BFD ATCH 113 IEL MILL LYS 7 1.245 1.00 0.00 BFD ATCH 113 IEL MILL LYS 7 1.245 1.00 0.00 BFD ATCH 113 IEL MILL LYS 7 1.245 1.00 0.00 BFD ATCH 113 IEL MILL LYS 7 1.245 1.00 0.00 BFD ATCH 113 IEL MILL LYS 7 1.245 1.00 0.00 BFD ATCH 113 IEL MILL LYS 7 1.245 1.00 0.00 BFD ATCH 113 IEL MILL LYS 7 1.245 1.00 0.00 BFD ATCH 113 IEL MILL LYS 7 1.245 1.00 0.00 BFD ATCH 113 IEL MILL LYS 7 1.245 1.00 0.00 BFD ATCH 113 IEL MILL LYS 7 1.245 1.00 0.00 BFD ATCH 113 IEL MILL LYS 7 1.245 1.00 0.00 BFD ATCH 113 IEL MILL LYS 7 1.245 1.00 0.00 BFD ATCH 113 I	117	11.546		8	8 .	BrD ATOM	1	9	r z		: :
1.144 1.00 0.00 BPD ATCH 10.141 LTS 6 0.333 1.00 0.00 BPD ATCH 10.141 LTS 6 1.345 1.00 0.00 BPD ATCH 10.141 LTS 6 1.345 1.00 0.00 BPD ATCH 10.141 LTS 1.45 1.453 1.00 0.00 BPD ATCH 10.10 LTS 1.45 1.453 1.00 0.00 BPD ATCH 11.10 0.11 1.45 1.453 1.00 0.00 BPD ATCH 11.10 0.11 1.45 1.453 1.00 0.00 BPD ATCH 11.10 0.11 1.45 1.454 1.00 0.00 BPD ATCH 11.10 0.11 1.45 1.455 1.00 0.00 BPD ATCH 11.10 ADL 11.10 1.455	909	12.034		8	9.0	BrD ATOM	20	8	LYS	•	77
1.144 1.00 0.00 BED ATCH 104 HEE LEN 6 2.125 1.00 0.00 BED ATCH 105 HE LEN 6 2.145 1.00 0.00 BED ATCH 105 HE LEN 6 2.145 1.00 0.00 BED ATCH 110 0.12 HE LEN 6 2.145 1.00 0.00 BED ATCH 110 0.12 HE LEN 6 2.145 1.00 0.00 BED ATCH 110 0.12 HE LEN 6 2.145 1.00 0.00 BED ATCH 111 H 0.12 1 2.145 1.00 0.00 BED ATCH 111 H 0.12 1 2.145 1.00 0.00 BED ATCH 111 H 0.12 1 2.145 1.00 0.00 BED ATCH 111 H 0.12 1 2.145 1.00 0.00 BED ATCH 111 H 0.12 1 2.145 1.00 0.00 BED ATCH 112 HE NO. 1 2.145 1.00 0.00 BED ATCH 113 H 0.12 1 2.145 1.00 0.00 BED ATCH 113 H 0.12 1 2.145 1.00 0.00 BED ATCH 113 H 0.12 1 2.145 1.00 0.00 BED ATCH 113 H 0.12 1 2.145 1.00 0.00 BED ATCH 113 H 0.12 1 2.145 1.00 0.00 BED ATCH 113 H 0.12 1 2.145 1.00 0.00 BED ATCH 113 H 0.12 1 2.145 1.00 0.00 BED ATCH 113 H 0.12 1 2.145 1.00 0.00 BED ATCH 113 H 0.12 1 2.145 1.00 0.00 BED ATCH 113 H 0.12 1 2.145 1.00 0.00 BED ATCH 113 H 0.12 1 2.145 1.00 0.00 BED ATCH 113 H 0.12 1 2.145 1.00 0.00 BED ATCH 113 H 0.12 1 2.145 1.00 0.00 BED ATCH 113 H 0.12 1 2.145 1.00 0.00 BED ATCH 113 H 0.12 1 2.145 1.00 0.00 BED ATCH 113 H 0.12 1 2.145 1.00 0.00 BED ATCH 113 H 0.12 1 2.145 1.00 0.00 BED ATCH 113 H 0.12 1 2.145 1.00 0.00 BED ATCH 113 H 0.12 1 2.145 1.00 0.00 BED ATCH 113 H 0.12 1 2.145 1.00 0.00 BED ATCH 113 H 0.12 1 2.145 1.00 0.00 BED ATCH 113 H 0.12 1 2.145 1.00 0.00 BED ATCH 113 H 0.12 1 2.145 1.00 0.00 BED ATCH 113 H 0.12 1 2.145 1.00 0.00 BED ATCH 113 H 0.13 H 0	521	13.203		8	9.0	BrD ATOM	9	H	LYS		1
2.152 1.00 0.00 BED ATCH 103 ME LESS 4 2.165 1.00 0.00 BED ATCH 103 ME LESS 4 2.165 1.00 0.00 BED ATCH 103 ME LESS 4 2.165 1.00 0.00 BED ATCH 103 ME LESS 4 2.165 1.00 0.00 BED ATCH 110 0 LESS 4 2.165 1.00 0.00 BED ATCH 110 0 LESS 4 2.165 1.00 0.00 BED ATCH 110 0 LESS 4 2.165 1.00 0.00 BED ATCH 110 0 LESS 4 2.165 1.00 0.00 BED ATCH 110 0 LESS 4 2.165 1.00 0.00 BED ATCH 110 ME DEL	513	13.088		8	0.0	BrD ATON	104	HE2	LYB	•	2
1.112 1.00 0.00 BED ATCH 112 112 112 112 112 112 112 112 112 11	250	13.953		8	8 :	BrD ATON	103	2	FXS	•	ä
1.124 1.100 0.000	591	13.65		8 8	8 8	aro Aron	9 5	1	9 Y	•	ž
14119 1.00 0.00 BFD ATOM 110 0 LVE 1 15151 1.00 0.00 BFD ATOM 111 0 LVE 1 15151 1.00 0.00 BFD ATOM 111 0 LVE 1 15151 1.00 0.00 BFD ATOM 111 10 C LVE 1 15151 1.00 0.00 BFD ATOM 111 10 C LVE 1 15151 1.00 0.00 BFD ATOM 111 10 BFD CLU 1 15151 1.00 0.00 BFD ATOM 111 10 BFD CLU 1 15151 1.00 0.00 BFD ATOM 111 10 BFD CLU 1 15151 1.00 0.00 BFD ATOM 112 BFD CLU 1 15151 1.00 0.00 BFD ATOM 112 BFD CLU 1 15151 1.00 0.00 BFD ATOM 112 BFD CLU 1 15151 1.00 0.00 BFD ATOM 112 BFD CLU 1 15151 1.00 0.00 BFD ATOM 112 BFD CLU 1 15151 1.00 0.00 BFD ATOM 112 BFD CLU 1 15151 1.00 0.00 BFD ATOM 112 BFD CLU 1 15151 1.00 0.00 BFD ATOM 112 BFD CLU 1 15151 1.00 0.00 BFD ATOM 112 BFD CLU 1 15151 1.00 0.00 BFD ATOM 112 BFD CLU 1 15151 1.00 0.00 BFD ATOM 112 BFD CLU 1 15151 1.00 0.00 BFD ATOM 112 BFD CLU 1 15151 1.00 0.00 BFD ATOM 112 BFD CLU 1 15151 1.00 0.00 BFD ATOM 112 BFD CLU 1 15151 1.00 0.00 BFD ATOM 112 BFD CLU 1 15151 1.00 0.00 BFD ATOM 112 BFD CLU 1 15151 1.00 0.00 BFD ATOM 112 BFD CLU 1 15151 1.00 0.00 BFD ATOM 112 BFD CLU 1 15151 1.00 0.00 BFD ATOM 112 BFD CLU 1 15151 1.00 0.00 BFD ATOM 112 BFD CLU 1 15151 1.00 0.00 BFD ATOM 112 BFD CLU 1 15151 1.00 0.00 BFD ATOM 112 BFD CLU 1 15151 1.00 0.00 BFD ATOM 112 BFD CLU 1 15151 1.00 0.00 BFD ATOM 112 BFD CLU 1 15151 1.00 0.00 BFD ATOM 112 BFD CLU 1 15151 1.00 0.00 BFD ATOM 112 BFD CLU 1 15151 1.00 0.00 BFD ATOM 112 BFD CLU 1 15151 1.00 0.00 BFD ATOM 112 BFD CLU 1 15151 1.00 0.00 BFD ATOM 112 BFD CLU 1 15151 1.00 0.00 BFD ATOM 112 BFD CLU 1 15151 1.00 0.00 BFD ATOM 112 BFD CLU 1 15151 1.00 0.00 BFD ATOM 112 BFD CLU 1 15151 1.00 0.00 BFD ATOM 112 BFD CLU 1 15151 1.00 0.00 BFD ATOM 112 BFD CLU 1 15151 1.00 0.00 BFD ATOM 112 BFD CLU 1 15151 1.00 0.00 BFD ATOM 112 BFD CLU 1 15151 1.00 0.00 BFD ATOM 112 BFD CLU 1 15151 1.00 0.00 BFD ATOM 112 BFD CLU 1 15151 1.00 0.00 BFD ATOM 112 BFD CLU 1 15151 1.00 0.00 BFD ATOM 112 BFD CLU 1 15151 1.00 0.00 BFD ATOM 112 BFD CLU 1 15151 1.00 0.00 BFD ATOM 112 BFD CLU 1 15151 1.00 0.00 BFD ATOM 112 BFD CLU 1 15151 1.00 0.00 BFD ATOM 112 BFD CLU 1 15151 1.00 0.	())	13.57		3 8	3 8	Bro Atom		2 2	2 2		į
1.651 1.100 0.000 BED ATUN HILL 1.100 0.000	197	14.632	1 69 1.	8	8	BrD ATOM	9		. S.		2
	2 :			0	8	BED ATOM	011	9	X8	•	=
1,114   1,100   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,00	123			0	8	BrD ATON	=	2	3	-	20.4
	256			2 9	2 3	Bro ATOM	3	o : 3 :	3 :	٠,	7
1581   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100				9 9	8 8	Bro After	3	o i	3 :	٠,	2 2
1.1441. 1.100 0.00 BED ATOM ATOM ATOM ATOM ATOM ATOM ATOM ATOM	120			2 2	3 8	Brb Aton		9 6 ≨ 8	3 3		
10   10   10   10   10   10   10   10	22			9	8	Brb ATOM	31	MB1 G	3	_	=
100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100	707			9 9	8 8	Brb ATON	::	200	3 :	۲,	=
	4.2			2 9	2 2	ATOM CERT	:	99	3 3	۰.	
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2.770 1.00 0.00 BFG ATON 1.00 0.	. 70\$	6.458 -3.	004 1.6	9	8	BrD ATON	171	HB2 P.	8		17.
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2.025 1.00 0.00 BED ATON 0.275 1.00 0.00 BED A		6.895 -2.	0.1 7.0	0	00.	BrD ATOM	3	103	8		19.6
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0.274 1.00 0.00 BED ATON 1.00 0.	<b>5</b>	7.825 -2.	026 1.6	0	8.	BrD ATOM	115	8	8	•	5
0.223 1.00 0.00 BED ATON 0.243 1.00 0.00 BED ATON 0.117 1.00 0.00 BED ATON 0.124 1.00 0.00 BED ATON 0.217 1.00 0.00 BED A	006	6.155 -0.	784 1.0	0	00	BrD ATOM	116	100	9		20.5
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-6.791 1.00 0.00 BrD ATDM 1-5.952 1.00 0.00 BrD ATDM 4.442 1.00 0.00 BrD ATDM 1-4.006 1.00 0.00 BrD ATDM 1-4.006 1.00 0.00	099.9	4.728 -5.	963 1.0	0	00	Bro ATOM	1 154	4 37	2		
	6.245	4.289 -6.	797 1.0	0	8	BrD ATON	155	7	2		
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